

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2005, 17:23:41 ; Search time 187.176 Seconds  
(without alignments)  
5979.480 Million cell updates/sec

Title: US-09-830-144-1\_COPY\_408\_1091

Perfect score: 684  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	1788	3	US-09-529-279-14
2	684	100.0	1788	4	US-10-158-895-14
3	684	100.0	2656	2	US-08-685-625A-5
4	684	100.0	2656	3	US-09-529-279-3
5	684	100.0	2656	4	US-10-158-895-3
6	684	100.0	2769	4	US-09-949-016-4031
7	585.4	85.6	2443	2	US-08-685-625A-1
8	141.2	20.6	76264	4	US-09-949-016-15773
9	104	15.2	507	4	US-09-270-767-106
10	104	15.2	507	4	US-09-270-767-15388
11	72	10.5	601	4	US-09-949-016-142616
12	54.6	8.0	426	4	US-09-513-999C-3587
13	54.6	8.0	1365	3	US-09-221-235-6
14	54.6	8.0	1365	3	US-09-221-928-6
15	54.6	8.0	1365	3	US-09-221-527-6
16	54.6	8.0	1365	3	US-09-221-236-6
17	54.6	8.0	1365	3	US-09-221-416-6
18	54.6	8.0	1365	3	US-09-221-245-6
19	54.6	8.0	1365	3	US-09-163-115-6
20	54.6	8.0	1365	3	US-09-221-528-6
21	54.6	8.0	1365	3	US-09-593-553-6
22	54.6	8.0	1365	3	US-09-221-237-6
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25	54.6	8.0	2120	3	US-09-221-235-4
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27	54.6	8.0	2120	3	US-09-221-527-4

28	54.6	8.0	2120	3	US-09-221-236-4	Sequence 4, Appli
29	54.6	8.0	2120	3	US-09-221-416-4	Sequence 4, Appli
30	54.6	8.0	2120	3	US-09-221-245-4	Sequence 4, Appli
31	54.6	8.0	2120	3	US-09-163-115-4	Sequence 4, Appli
32	54.6	8.0	2120	3	US-09-221-528-4	Sequence 4, Appli
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38	52	7.6	1251	3	US-09-468-442-2	Sequence 2, Appli
39	52	7.6	1353	2	US-09-211-930-8	Sequence 8, Appli
40	52	7.6	1353	3	US-09-340-993-8	Sequence 8, Appli
41	52	7.6	1353	3	US-09-468-442-8	Sequence 8, Appli
42	52	7.6	1542	4	US-09-345-473B-13	Sequence 13, Appli
43	52	7.6	3201	2	US-09-211-930-1	Sequence 1, Appli
44	52	7.6	3201	3	US-09-340-993-1	Sequence 1, Appli
45	52	7.6	3201	3	US-09-468-442-1	Sequence 1, Appli

#### ALIGNMENTS

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RESULT 1
US-09-529-279-14
; Sequence 14, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIO
; APPLICANT: TSUCHIYA, MAYUKI
; TITLE OR INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-09-529-279-14
Query Match 100.0%; Score 684; DB 3; Length 1788;
Best local Similarity 100.0%; Pred. No. 1.1e-217;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAGAGCTTGGCGAGTATCCGCTGTAACCATCTAATATGTAAGCTTATGAGCC 60
232 GTAGAGCTTGGCGAGTATCCGCTGTAACCATCTAATATGTAAGCTTATGAGCC 291
61 TGGTGAATCAGTGTGCTGTGTATGTAATGTAATGTAAGGAGGCTCTTTATATATG 120
292 TGGTGAATCAGTGTGCTGTGTATGTAATGTAATGTAAGGAGGCTCTTTATATATG 351
121 CTGATGATGCTGAACCATTCATTAATATCTGTGCCACGCAATGATGCTGTTA 180
352 CTGATGATGCTGAACCATTCATTAATATCTGTGCCACGCAATGATGCTGTTA 411
181 CAGGTTCAGGAGGAGGCTTATCTTCAAGCATGCAACCAAGGCTTATTCACAGG 240
412 CAGGTTCAGGAGGAGGCTTATCTTCAAGCATGCAACCAAGGCTTATTCACAGG 471
241 GACCTGAACCAACCACTTACTGTGTGTCAGGGGAGACAGTTCTAAATTTGTAT 300
472 GACCTGAACCAACCACTTACTGTGTGTCAGGGGAGACAGTTCTAAATTTGTAT 531
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QY 301 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTTGG 360  
Db 532 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTTGG 591  
QY 361 ATGGCAGCTGAAGTTTGAAGGTGTATTAACGTGAAATATGAGAGTCTTCACTGG 420  
Db 592 ATGGCAGCTGAAGTTTGAAGGTGTATTAACGTGAAATATGAGAGTCTTCACTGG 651  
QY 421 GGTATTAATCTTTGGAGAGTAAACGCGTCGAAACCTTTGATGATGTTGGGCCCA 480  
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QY 481 GCTTTCCGAATCATGTGGGCTGTATTAATGTACTCGACACCACTGATTAATAATTTA 540  
Db 712 GCTTTCCGAATCATGTGGGCTGTATTAATGTACTCGACACCACTGATTAATAATTTA 771  
QY 541 CCTAAGCCCATTTGAGAGCTGATGACTGTTGTTGCTTAAAGATCCTTCCAGCGCCT 600  
Db 772 CCTAAGCCCATTTGAGAGCTGATGACTGTTGTTGCTTAAAGATCCTTCCAGCGCCT 831  
QY 601 TCAATGAGGAATTTGTGAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 660  
Db 832 TCAATGAGGAATTTGTGAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 891  
QY 661 GAGCCATTACAGTATCTTGTTCAG 684  
Db 892 GAGCCATTACAGTATCTTGTTCAG 915

## RESULT 2

US-10-158-895-14  
; Sequence 14, Application US/10158895  
; Patent No. 6551840  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158, 895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529, 279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ. ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ. ID NO 14  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(1776)  
US-10-158-895-14

Query Match 100.0%; Score 684; DB 4; Length 1788;  
Best Local Similarity 100.0%; Pred. No. 1.1e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGAGTTATCCGTGTGAACCAATCTTAATATGTAAAGCTTATGAGCC 60  
Db 232 GTAGAGCTTGGGAGTTATCCGTGTGAACCAATCTTAATATGTAAAGCTTATGAGCC 291  
QY 61 TCGTTGAATCCAGTGTGCTGTGATGAAATATGCTGAAGGGGCTCTTATATATATGTG 120  
Db 292 TCGTTGAATCCAGTGTGCTGTGATGAAATATGCTGAAGGGGCTCTTATATATATGTG 351  
QY 121 CTGCATGTGTGAACCAATTCATATTAATGCTGCGCCAGCAATGATGGTGTTA 180

Db 352 CTGCATGTGTGAACCAATTCATATTAATGCTGCGCCAGCAATGATGGTGTTA 411  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATCAACCAAGCGCTTAATTCACAG 240  
Db 412 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATCAACCAAGCGCTTAATTCACAG 471  
QY 241 GACCTGAACCAACCAATCTTACGTGTGTGTCAGGGGGGACAGTTCTAATAATTTGTGAT 300  
Db 472 GACCTGAACCAACCAATCTTACGTGTGTGTCAGGGGGGACAGTTCTAATAATTTGTGAT 531  
QY 301 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTTGG 360  
Db 532 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTTGG 591  
QY 361 ATGGCAGCTGAAGTTTGAAGGTGTATTAACGTGAAATATGAGAGTCTTCACTGG 420  
Db 592 ATGGCAGCTGAAGTTTGAAGGTGTATTAACGTGAAATATGAGAGTCTTCACTGG 651  
QY 421 GGTATTAATCTTTGGAGAGTAAACGCGTCGAAACCTTTGATGATGTTGGGCCCA 480  
Db 652 GGTATTAATCTTTGGAGAGTAAACGCGTCGAAACCTTTGATGATGTTGGGCCCA 711  
QY 481 GCTTTCCGAATCATGTGGGCTGTATTAATGTACTCGACACCACTGATTAATAATTTA 540  
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Db 772 CCTAAGCCCATTTGAGAGCTGATGACTGTTGTTGCTTAAAGATCCTTCCAGCGCCT 831  
QY 601 TCAATGAGGAATTTGTGAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 660  
Db 832 TCAATGAGGAATTTGTGAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 891  
QY 661 GAGCCATTACAGTATCTTGTTCAG 684  
Db 892 GAGCCATTACAGTATCTTGTTCAG 915

## RESULT 3

US-08-685-625A-5  
; Sequence 5, Application US/08685625A  
; Patent No. 5945301  
; GENERAL INFORMATION:  
; APPLICANT: UENO, Naoto  
; APPLICANT: MATSUMOTO, Kunihiko  
; APPLICANT: IRIE, Kenji  
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION SYSTEM  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685, 625A  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-253549  
; FILING DATE: 29-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36, 607  
; REFERENCE/DOCKET NUMBER: 001560-267

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2656 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..1922  
US-08-685-625A-5

Query Match 100.0%; Score 684; DB 2; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1,4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGCGAGTATCCCGGTGTAACCATCTAATATTGTAAGCTTTATGAGCC 60  
DB 408 GTAGAGCTTGGGCGAGTATCCCGGTGTAACCATCTAATATTGTAAGCTTTATGAGCC 467  
QY 61 TGTGTAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120  
DB 468 TGTGTAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 527  
QY 121 CTGATGATGCTGTAACCATCTGCAATATTATATCTGCTCCACGCAATGATGTTGTTTA 180  
DB 528 CTGATGATGCTGTAACCATCTGCAATATTATCTGCTCCACGCAATGATGTTGTTTA 587  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAACG 240  
DB 588 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAACG 647  
QY 241 GACCTGAACCAACCAACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTTGAT 300  
DB 648 GACCTGAACCAACCAACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTTGAT 707  
QY 301 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 360  
DB 708 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 767  
QY 361 ATGCACTGTAAGTTTGAAGGTATTAAGTGAATAATGTAAGTCTTCAAGCTGG 420  
DB 768 ATGCACTGTAAGTTTGAAGGTATTAAGTGAATAATGTAAGTCTTCAAGCTGG 827  
QY 421 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGATGTTGGGCCA 480  
DB 828 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGATGTTGGGCCA 887  
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DB 888 GCTTCCGAATCATGAGGCTGTTCATATATGTACTGACCAACCACTGATTAATAATTTA 947  
QY 541 CTTAAGCCATTGAGAGCTGTATGATCTGTTGTTGTTAAAGATCTTCCAGGCGCT 600  
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QY 601 TCAATGAGGAATTTGTAATAATATGACTCACTTGATGCGGTACTTTCAGAGACAGAT 660  
DB 1008 TCAATGAGGAATTTGTAATAATATGACTCACTTGATGCGGTACTTTCAGAGACAGAT 1067  
QY 661 GAGCATTACAGTATCTTGTGAG 684  
DB 1068 GAGCATTACAGTATCTTGTGAG 1091

RESULT 4  
US-09-529-279-3  
Sequence 3, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OR INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3

LENGTH: 2656  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (183)..(1919)  
US-09-529-279-3

Query Match 100.0%; Score 684; DB 3; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1,4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGAGCTTGGGCGAGTATCCCGGTGTAACCATCTAATATTGTAAGCTTTATGAGCC 60  
DB 408 GTAGAGCTTGGGCGAGTATCCCGGTGTAACCATCTAATATTGTAAGCTTTATGAGCC 467  
QY 61 TGTGTAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120  
DB 468 TGTGTAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 527  
QY 121 CTGATGATGCTGTAACCATCTGCAATATTATATCTGCTCCACGCAATGATGTTGTTTA 180  
DB 528 CTGATGATGCTGTAACCATCTGCAATATTATCTGCTCCACGCAATGATGTTGTTTA 587  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAACG 240  
DB 588 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATCAACG 647  
QY 241 GACCTGAACCAACCAACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTTGAT 300  
DB 648 GACCTGAACCAACCAACTTACTGCTGTTGCAAGGGGCAAGTCTTAAATTTTGAT 707  
QY 301 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 360  
DB 708 TTTGTAACGCTGTGACATTCAACACATGACCAATTAACAAGGAGTGTCTGG 767  
QY 361 ATGCACTGTAAGTTTGAAGGTATTAAGTGAATAATGTAAGTCTTCAAGCTGG 420  
DB 768 ATGCACTGTAAGTTTGAAGGTATTAAGTGAATAATGTAAGTCTTCAAGCTGG 827  
QY 421 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGATGTTGGGCCA 480  
DB 828 GGTATTAATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGATGTTGGGCCA 887  
QY 481 GCTTCCGAATCATGAGGCTGTTCATATATGTACTGACCAACCACTGATTAATAATTTA 540  
DB 888 GCTTCCGAATCATGAGGCTGTTCATATATGTACTGACCAACCACTGATTAATAATTTA 947  
QY 541 CTTAAGCCATTGAGAGCTGTATGATCTGTTGTTGTTAAAGATCTTCCAGGCGCT 600  
DB 948 CTTAAGCCATTGAGAGCTGTATGATCTGTTGTTGTTAAAGATCTTCCAGGCGCT 1007  
QY 601 TCAATGAGGAATTTGTAATAATATGACTCACTTGATGCGGTACTTTCAGAGACAGAT 660  
DB 1008 TCAATGAGGAATTTGTAATAATATGACTCACTTGATGCGGTACTTTCAGAGACAGAT 1067  
QY 661 GAGCATTACAGTATCTTGTGAG 684  
DB 1068 GAGCATTACAGTATCTTGTGAG 1091

RESULT 5  
US-10-158-895-3  
; Sequence 3, Application US/10158895  
; Patent No. 6551840  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2656  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (183)..(1919)  
US-10-158-895-3

Query Match 100.0%; Score 684; DB 4; Length 2656;  
Best Local Similarity 100.0%; Pred. No. 1,4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTAAAGCTTGGGCGATTATCCGTTGAACCATCTAATATGTAAGCTTTATGAGCC 60
DB 408 GTAAAGCTTGGGCGATTATCCGTTGAACCATCTAATATGTAAGCTTTATGAGCC 467
QY 61 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATATATG 120
DB 468 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATATATG 527
QY 121 CTGCATGCTGTAACCATTCATATATATATGCTGCCACCAATGAGTGTGTTA 180
DB 528 CTGCATGCTGTAACCATTCATATATATATGCTGCCACCAATGAGTGTGTTA 587
QY 181 CAGGTTCACCAAGAGTGGCTTATCTTCAACATGCAACCCAAAGCGTTAATCAAG 240
DB 588 CAGGTTCACCAAGAGTGGCTTATCTTCAACATGCAACCCAAAGCGTTAATCAAG 647
QY 241 GACCTGAACCAACCACTTACTGCTGTGACAGGGGGGACAGTTTAAATAATTTGTAT 300
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DB 1008 TCAATGAGGAAATTTGAAATATATGACTGATGCGGATCTTCCAGAGAGAT 1067
QY 661 GAGCCATTACATATCTTGTGAG 684
DB 1068 GAGCCATTACATATCTTGTGAG 1091
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RESULT 6  
US-09-949-016-4031  
; Sequence 4031, Application US/09949016  
; Patent No. 6812338  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4031  
; LENGTH: 2769  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-4031

Query Match 100.0%; Score 684; DB 4; Length 2769;  
Best Local Similarity 100.0%; Pred. No. 1,4e-217;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTAAAGCTTGGGCGATTATCCGTTGAACCATCTAATATGTAAGCTTTATGAGCC 60
DB 388 GTAAAGCTTGGGCGATTATCCGTTGAACCATCTAATATGTAAGCTTTATGAGCC 447
QY 61 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATATATG 120
DB 448 TGCTTGAATCCAGTGTCTTGTGATGAATATGCTGAAGGGGCTTTATATATATG 507
QY 121 CTGCATGCTGTAACCATTCATATATATATGCTGCCACCAATGAGTGTGTTA 180
DB 508 CTGCATGCTGTAACCATTCATATATATATGCTGCCACCAATGAGTGTGTTA 567
QY 181 CAGGTTCACCAAGAGTGGCTTATCTTCAACATGCAACCCAAAGCGTTAATCAAG 240
DB 568 CAGGTTCACCAAGAGTGGCTTATCTTCAACATGCAACCCAAAGCGTTAATCAAG 627
QY 241 GACCTGAACCAACCACTTACTGCTGTGACAGGGGGGACAGTTTAAATAATTTGTAT 300
DB 628 GACCTGAACCAACCACTTACTGCTGTGACAGGGGGGACAGTTTAAATAATTTGTAT 687
QY 301 TTGTGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTGTTG 360
DB 688 TTGTGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGGAGTGTGTTG 747
QY 361 ATGGCACTGAAGTTTGAAGGTAGTAATTAAGTAAGAAATGTGACGTTTCAGCTGG 420
DB 748 ATGGCACTGAAGTTTGAAGGTAGTAATTAAGTAAGAAATGTGACGTTTCAGCTGG 807
QY 421 GGTATATATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 480
DB 808 GGTATATATCTTTGGGAAGTATACGCGTGGAAACCTTTGATGAGATTGTGGCCA 867
QY 481 GCTTCCGATATGAGGCTGTGATATATGTAATTCGACCCGCTGATTAATAATTTA 540
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Db 868 GCTTCGAATCATGAGGCTGTCTCATATGTAATGACCAACCACTGATATAAAATTTA 927  
Qy 541 CCTAAGCCATTGAGAGCTGTATGCTGTGTGTAAAGATCCCTCCAGAGCCCT 600  
Db 928 CCTAAGCCATTGAGAGCTGTATGCTGTGTGTAAAGATCCCTCCAGAGCCCT 987  
Qy 601 TCAATGAGAGAAATTTGAAATATATGACTCACTTGATCGGTACTTTCCAGAGCAGAT 660  
Db 988 TCAATGAGAGAAATTTGAAATATATGACTCACTTGATCGGTACTTTCCAGAGCAGAT 1047  
Qy 661 GAGCCATTACAGTATCCTTGTGAG 684  
Db 1048 GAGCCATTACAGTATCCTTGTGAG 1071

RESULT 7  
US-08-685-625A-1

; Sequence 1, Application US/08685625A  
; Patent No. 5945301  
; GENERAL INFORMATION:  
; APPLICANT: UENO, Naoto  
; APPLICANT: MATSUMOTO, Kunihiko  
; APPLICANT: IRIE, Kenji  
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL  
; TITLE OF INVENTION: TRANSDUCTION SYSTEM  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/685,625A  
; FILING DATE: 24-JUL-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-253549  
; FILING DATE: 29-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuch, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 001560-267  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2443 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 157..1893  
; US-08-685-625A-1

## Query Match 85.6%; Score 585.4; DB 2; Length 2443;

Best Local Similarity 91.1%; Pred. No. 1.1e-184;  
Matches 622; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 1 GTAGAGCTTCGCGACGTATCCCGTGTGAACCATCTAATATGTAAAGCTTTATGAGCC 60  
Db 382 GTGAGAGCTTCGCGACGTATCCCGTGTGAACCATCTAATATGTCAAGTTGTACGAGCC 441

Qy 61 TGCTGAATCCAGTGTGTCTTGTGATGATATGCTGAAGGGGGCTTTATATATATG 120  
Db 442 TGCTGAATCCAGTGTGTCTTGTGATGATATGCTGAAGGGGGCTTTATATATATG 501  
Qy 121 CTGATGATGCTGTAACCATGACCATATATATATGCTGCTGCCAAGGATGTGGGTTA 180  
Db 502 CTGATGATGCTGTAACCATGACCATATATATATGCTGCTGCCAAGGATGTGGGTTA 561  
Qy 181 CAGTGTCCCAAGGAGTGTGCTTATCTTCAAGCATGCAACCCAAAGGCTTAATCACAG 240  
Db 562 CAGTGTCCCAAGGAGTGTGCTTATCTTCAAGCATGCAACCCAAAGGCTTAATCACAG 621  
Qy 241 GACCTGAACCAACCACTTACTGCTGCTGAGGGGGGAGCTTAAAAATTTGTAT 300  
Db 622 GACCTGAACCTCCAACTTCTGCTGCTGCTGAGGGGAGCTTAAAAATTTGTAT 681  
Qy 301 TTTGTACAGCTGTGTGATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTG 360  
Db 682 TTTGTACAGCTGTGTGATTCAGACACATGACCAATTAACAGGGGAGTGTGCTTG 741  
Qy 361 ATGGACCTGAGTTTGAAGGTATTAATTAAGTGAAGGAAATGAGCTTCAAGCTG 420  
Db 742 ATGGACCTGAGTTTGAAGGTATTAATTAAGTGAAGGAAATGAGCTTCAAGCTG 801  
Qy 421 GGTATTAATCTTGTGGAAGTATACGCGTGGAAACCTTTGATGATGATGTGGCCCA 480  
Db 802 GGTATTAATCTTGTGGAAGTATACGCGTGGAAACCTTTGATGATGATGTGGCCCA 861  
Qy 481 GCTTTCGATATGATGAGGCTGTGCTGATATATGATCTGACACCACTGATATAAATTTA 540  
Db 862 GCTTTCGATATGATGAGGCTGTGCTGATATATGATCTGACACCACTGATATAAATTTA 921  
Qy 541 CCTAAGCCATTGAGAGCTGTATGATCTGTTGTGTAAAGATCCCTCCAGAGCCCT 600  
Db 922 CCTAAGCCATTGAGAGCTGTATATGACGCTGTGTGTAAAGATCCCTCCAGAGCCCT 981  
Qy 601 TCAATGAGAGAAATTTGAAATATATGACTCACTTGATCGGTACTTTCCAGAGCAGAT 660  
Db 982 TCAATGAGAGAAATTTGAAATATATGACTCACTTGATCGGTACTTTCCAGAGCAGAT 1041  
Qy 661 GAGCCATTACAGTATCCTTGTGCA 683  
Db 1042 GAGCCATTACAGTATCCTTGTGCA 1064

## RESULT 8

US-09-949-016-15773  
; Sequence 15773, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1601307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15773  
; LENGTH: 76264  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(76264)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15773

Query Match 20.6%; Score 141.2; DB 4; Length 7624;  
 Best Local Similarity 97.9%; Pred. No. 1.8e-35;  
 Matches 143; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 118 GTGCTGACAGTGTGCTGAACCATTTGCTATTTACTGCTGCCACGCAATGATGTTGTGT 177  
 DB 28834 GTGCTGACAGTGTGCTGAACCATTTGCTATTTACTGCTGCCACGCAATGATGTTGTGT 28893  
 QY 178 TTACAGTGTTCCTCAAGAGTGTGCTTATCTTCAACAGTGAACCCAAAGCGCTAATTGAC 237  
 DB 28894 TTACAGTGTTCCTCAAGAGTGTGCTTATCTTCAACAGTGAACCCAAAGCGCTAATTGAC 28953  
 QY 238 AGGAGCTGAAACCCCAACTTACT 263  
 DB 28954 AGGAGCTGAAACCCCAACTTACT 28979

## RESULT 9

US-09-270-767-106/c  
 ; Sequence 106, Application US/09270767  
 ; Patent No. 6703491

; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 106  
 ; LENGTH: 507  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-106

Query Match 15.2%; Score 104; DB 4; Length 507;  
 Best Local Similarity 58.9%; Pred. No. 2.9e-24;  
 Matches 198; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 346 GGGAGTCTGCTGGTGGATGGACCTGAAGTTTGAAGTATATTAAGTGAAGAAATGT 405  
 DB 501 GGTATTCGCCCTTGATGAGCGCCGAGAGCTTGGAAAGCTCCAAAGTATAGGAAATGT 442  
 QY 406 GAGCTCTGAGCTGGGGTATTTATCTTGGGAAGTAAAGCGGTGGAAACCTTTGAT 465  
 DB 441 GACATTTTCAAGCTGGGCAATGTTCTATGGAAGTCTGTCCAGAAAGCGCTTTAA 382  
 QY 466 GAGATGTGTGCGCCAGCTTCCGAATCATGTGGGCTGTTCAATATGTTACTGACCA 525  
 DB 381 GGCAT---CGACAATGCTACACATTCAGTGAAGAAATCTACAGAGTGAAGCCCGCG 325  
 QY 526 CTGATAAAAATTTACTTAAGCCCATGAGAGCTGATGACTGTTGTTGTTAAAGAT 585  
 DB 324 CTGCTGACCACTTGCCCAAGCCCATGAGAGCTGATGACTGCTGCTGGAAGAAAGCGTG 265  
 QY 586 CTTCCAGAGCGCTTCAATGAGAGAAATTTGAAATATATGACTCACTTATGCGGTAC 645  
 DB 264 CCGAGAGATGCGCGTGTGATGACATATGATGAGGCTTATGACGAGATCTGCAAGGAC 205  
 QY 646 TTTCAGAGACAGATGAGCATTAAGTATCTTGT 681  
 DB 204 TATACGGGGCGGACAAAGCGCTGAAATACACTTT 169

## RESULT 10

US-09-270-767-15388/c  
 ; Sequence 15388, Application US/09270767  
 ; Patent No. 6703491

; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 15388  
 ; LENGTH: 507  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster  
 US-09-270-767-15388

Query Match 15.2%; Score 104; DB 4; Length 507;  
 Best Local Similarity 58.9%; Pred. No. 2.9e-24;  
 Matches 198; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 346 GGGAGTCTGCTGGTGGATGGACCTGAAGTTTGAAGTATATTAAGTGAAGAAATGT 405  
 DB 501 GGTATTCGCCCTTGATGAGCGCCGAGAGCTTGGAAAGCTCCAAAGTATAGGAAATGT 442  
 QY 406 GAGCTCTGAGCTGGGGTATTTATCTTGGGAAGTAAAGCGGTGGAAACCTTTGAT 465  
 DB 441 GACATTTTCAAGCTGGGCAATGTTCTATGGAAGTCTGTCCAGAAAGCGCTTTAA 382  
 QY 466 GAGATGTGTGCGCCAGCTTCCGAATCATGTGGGCTGTTCAATATGTTACTGACCA 525  
 DB 381 GGCAT---CGACAATGCTACACATTCAGTGAAGAAATCTACAGAGTGAAGCCCGCG 325  
 QY 526 CTGATAAAAATTTACTTAAGCCCATGAGAGCTGATGACTGTTGTTGTTAAAGAT 585  
 DB 324 CTGCTGACCACTTGCCCAAGCCCATGAGAGCTGATGACTGCTGCTGGAAGAAAGCGTG 265  
 QY 586 CTTCCAGAGCGCTTCAATGAGAGAAATTTGAAATATATGACTCACTTATGCGGTAC 645  
 DB 264 CCGAGAGATGCGCGTGTGATGACATATGATGAGGCTTATGACGAGATCTGCAAGGAC 205  
 QY 646 TTTCAGAGACAGATGAGCATTAAGTATCTTGT 681  
 DB 204 TATACGGGGCGGACAAAGCGCTGAAATACACTTT 169

## RESULT 11

US-09-949-016-142616/c  
 ; Sequence 142616, Application US/09949016  
 ; Patent No. 6812359

; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: CLO01307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 142616  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-142616

Query Match 10.5%; Score 72; DB 4; Length 601;  
 Best Local Similarity 84.4%; Pred. No. 1.5e-13;  
 Matches 81; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 AGAGCTTGCGAGTTATCCGCTGTGAACCATCTTAATATTTGAAGCTTATGAGCGTG 62  
 DB 96 ACAGCTTGCGAGTTATCCGCTGTGAACCATCTTAATATTTGAAGCTTATGAGCGTG 37  
 QY 63 CTGATTCAGTGTGCTTGTGATGAGATATGCTGA 98

Db 36 CTTGATCCAGTAGTTGTTACTTTTCATGTCGA 1

## RESULT 12

US-09-513-999C-3587  
; Sequence 3587, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513, 999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 3587  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..425  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 358  
; OTHER INFORMATION: m-a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 392  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 393  
; OTHER INFORMATION: b=c or g or t  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 119  
; OTHER INFORMATION: Xaa=Ala or Glu  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 131  
; OTHER INFORMATION: Xaa=Ala or Pro or Ser  
US-09-513-999C-3587

Query Match 8.0%; Score 54.6; DB 4; Length 426;  
Best Local Similarity 48.3%; Pred. No. 8.2e-08;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTCACAGCATGCA 219  
DB 15 CACATTATGACCTGGGCCACTGATGTAGCAAGAAAGATTCATTATTACATATGAGAGCT 74  
QY 220 CCCAAGGCGTAATTCACAGGAGCCTGAAACACCAAACTTACTGCTGGTTGACAGGGGG 279  
DB 75 CTTGTCAGAGTATTCACAGAGACCTCAAGTCAAGAAAGCTTATATAGCTCTGATGGA 134  
QY 280 ACAGTTCTAAAAATTTGTGATTTTGTATACAGCCTGTGACATTCAGACACATGACCAAT 339  
DB 135 GACTGAGAGATCTGACATTTGTGCTCTCGATTCATTAACATACACACATGATGCC 194  
QY 340 AACAGGGAGAGTCTGCTGATGAGACCTGAAAGTTTGAAGTAGTAAATTAACAGTGA 399  
DB 195 TTGGTTGAACTTTCCCATGAGATGGCTCAAGAAATTCACAGATCTCCCTGTGTCAGA 254  
QY 400 AAATGTGACGTTCTGACGTGGGGTATTTATCTTTGGGAAGTATTAACGCGTCGAAACCC 459  
DB 255 ACTGTGACACATATTCCTATGATGTGTTCTCTGGGAGATGTAACAAAGGAGGTCCCC 314

QY 460 TTGTGATGAGTTGGTGG 476  
DB 315 TTTAAAGTTTGGAGG 331

## RESULT 13

US-09-221-235-6  
; Sequence 6, Application US/09221235  
; Patent No. 6043040  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/221,235  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1365)  
US-09-221-235-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGCAATGAGTGGTGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTCACAGCATGCA 219  
DB 316 CACATTATGACCTGGGCCACTGATGTAGCAAGAAAGATTCATTATACATATGAGAGCT 375  
QY 220 CCCAAGGCGTAATTCACAGGAGCCTGAAACACCAAACTTACTGCTGGTTGACAGGGGG 279  
DB 376 CTTGTCAGAGTATTCACAGAGACCTCAAGTCAAGAAAGCTTATATAGCTCTGATGGA 435  
QY 280 ACAGTTCTAAAAATTTGTGATTTTGTATACAGCCTGTGACATTCAGACACATGACCAAT 339  
DB 436 GACTGAGAGATCTGACATTTGTGCTCTCGATTCATTAACATACACACATGATGCC 495  
QY 340 AACAGGGAGAGTCTGCTGATGAGACCTGAAAGTTTGAAGTAGTAAATTAACAGTGA 399  
DB 496 TTGGTTGAACTTTCCCATGAGATGGCTCAAGAAATTCACAGATCTCCCTGTGTCAGA 555  
QY 400 AAATGTGACGTTCTGACGTGGGGTATTTATCTTTGGGAAGTATTAACGCGTCGAAACCC 459  
DB 556 ACTGTGACACATATTCCTATGATGTGTTCTCTGGGAGATGTAACAAAGGAGGTCCCC 615  
QY 460 TTGTGATGAGTTGGTGG 476  
DB 616 TTTAAAGTTTGGAGG 632

## RESULT 14

US-09-221-928-6  
; Sequence 6, Application US/09221928  
; Patent No. 6121030  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/221,928  
; CURRENT FILING DATE: 1998-12-28  
; EARLIER APPLICATION NUMBER: 09/163,115  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6

LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-928-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGGAATGATGGTGTGTTACAGTGTCCCAAGAGTGGCTTATCTTCACAGATGCA 219  
DB 316 CACATTAATGACCTGGCCACATGATGACCAAGAAATGCAATTAATTAATATGAGGCT 375  
QY 220 CCCAAGCGCTAATTCACAGGAGCCTGAAACCAACCTAAGCGTGGTGGAGGGGG 279  
DB 376 CCTGTCAAGTGATTCACAGAGACTCTAAGTCAGAAACGTTTATAGCTGCTGATGA 435  
QY 280 ACAGTTCTAAAAATTTGTGATTTGTGACAGCTGTGACATTCAGACACATGACCAAT 339  
DB 436 GTACTGAGATCTGTGACTTTGTGCTCTGCTTCATACATACACACATGTC 495  
QY 340 AACAGGGAGTGTGCTGTGATGAGCACTGAAGTTTGTGAAGTATTAATACATGAA 399  
DB 496 TTGGTTGAATCTTCCATGATGAGCTCCAGAGTATCCAGAGTCTCCCTGTGTAGAA 555  
QY 400 AAATGTGACGCTTCAGCTGGGATATTCTTTGGAGATGATACGCGTCGAAACCC 459  
DB 556 ACTGTGACACATATTCCTATGATGTTGTTCTCTGGAGATGCTAACAGGAGGTCCC 615  
QY 460 TTTGATGAGATTGTGG 476  
DB 616 TTAAAGTTTGAAG 632

## RESULT 15

US-09-221-527-6  
Sequence 6, Application US/09221527  
Patent No. 6146832  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/221,527  
CURRENT FILING DATE: 1998-12-28  
EARLIER APPLICATION NUMBER: 09/163,115  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1365  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1365)  
US-09-221-527-6

Query Match 8.0%; Score 54.6; DB 3; Length 1365;  
Best Local Similarity 48.3%; Pred. No. 1.6e-07;  
Matches 153; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 160 CACGGAATGATGGTGTGTTACAGTGTCCCAAGAGTGGCTTATCTTCACAGATGCA 219  
DB 316 CACATTAATGACCTGGCCACATGATGACCAAGAAATGCAATTAATTAATATGAGGCT 375  
QY 220 CCCAAGCGCTAATTCACAGGAGCCTGAAACCAACCTAAGCGTGGTGGAGGGGG 279  
DB 376 CCTGTCAAGTGATTCACAGAGACTCTAAGTCAGAAACGTTTATAGCTGCTGATGA 435  
QY 280 ACAGTTCTAAAAATTTGTGATTTGTGACAGCTGTGACATTCAGACACATGACCAAT 339

DB 436 GTACTGAGATCTGTGACTTTGTTGCTCTCGGTTCCATACCATACACACATGTCC 495  
QY 340 AACAGGGAGTGTGCTGTGATGAGCACTGAAGTTTGTGAAGTATTAATACATGAA 399  
DB 496 TTGGTTGAATCTTCCATGATGAGCTCCAGAGTATCCAGAGTCTCCCTGTGTAGAA 555  
QY 400 AAATGTGACGCTTCAGCTGGGATATTCTTTGGAGATGATACGCGTCGAAACCC 459  
DB 556 ACTGTGACACATATTCCTATGATGTTGTTCTCTGGAGATGCTAACAGGAGGTCCC 615  
QY 460 TTTGATGAGATTGTGG 476  
DB 616 TTAAAGTTTGAAG 632

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OM nucleic - nucleic search, using sw model

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(Without alignments)  
6043.588 Million cell updates/sec

Title: US-09-830-144-1\_COPY\_408\_1091

Perfect score: 684  
Sequence: 1 gtgagcttcgcagctatc.....cattacagctatctgtcag 684

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Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*  
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20: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq.\*  
23: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*  
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26: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	684	100.0	1705	US-10-283-023-1	Sequence 1, Appli
2	684	100.0	1705	US-10-283-023-3	Sequence 3, Appli
3	684	100.0	1705	US-10-386-414-12	Sequence 12, Appli
4	684	100.0	1788	US-10-158-895-14	Sequence 14, Appli
5	684	100.0	1788	US-10-384-743-14	Sequence 14, Appli
6	684	100.0	2656	US-10-158-895-3	Sequence 3, Appli
7	684	100.0	2656	US-10-384-743-3	Sequence 3, Appli

8	684	100.0	2769	US-10-343-710-107	Sequence 107, App
9	65.4	9.6	1428	US-09-938-842A-882	Sequence 882, App
10	65.4	9.6	1428	US-09-938-842A-882	Sequence 882, App
11	64.4	9.4	2022	US-10-425-115-92866	Sequence 92866, A
12	61	8.9	1733	US-10-437-963-93253	Sequence 93253, A
13	56.8	8.3	476	US-09-732-627A-4894	Sequence 4894, Ap
14	56.6	8.3	1398	US-09-938-842A-633	Sequence 633, App
15	56.6	8.3	1398	US-09-938-842A-633	Sequence 633, App
16	56.2	8.2	732	US-10-767-701-10245	Sequence 10245, A
17	55.8	8.2	1953	US-10-424-599-53404	Sequence 53404, A
18	54.8	8.0	658	US-10-767-701-7653	Sequence 7653, Ap
19	54.6	8.0	863	US-10-425-114-6087	Sequence 6087, Ap
20	54.6	8.0	1063	US-10-106-698-2068	Sequence 2068, Ap
21	54.6	8.0	1365	US-09-757-982-6	Sequence 6, Appli
22	54.6	8.0	1365	US-10-786-501-6	Sequence 6, Appli
23	54.6	8.0	1456	US-10-425-114-36409	Sequence 36409, A
24	54.6	8.0	2119	US-10-352-674A-1	Sequence 1, Appli
25	54.6	8.0	2120	US-09-757-982-4	Sequence 4, Appli
26	54.6	8.0	2120	US-10-786-501-4	Sequence 4, Appli
27	54.6	8.0	2181	US-10-425-115-94149	Sequence 94149, A
28	54.6	8.0	2191	US-10-296-115-98	Sequence 98, Appli
29	54.6	8.0	2251	US-10-094-749-838	Sequence 838, App
30	54.6	8.0	2455	US-10-737-450-65	Sequence 65, Appli
31	54.6	8.0	3767	US-10-751-736-1	Sequence 1, Appli
32	54	7.9	782	US-10-425-114-18352	Sequence 18352, A
33	54	7.9	1926	US-10-425-114-34394	Sequence 22688, A
34	54	7.9	2029	US-10-425-114-34394	Sequence 34394, A
35	54	7.9	2050	US-10-425-115-84871	Sequence 84871, A
36	54	7.9	2793	US-10-425-115-16689	Sequence 16689, A
37	53.8	7.9	978	US-10-767-701-9215	Sequence 9215, Ap
38	53	7.7	1694	US-10-021-323-3324	Sequence 3324, Ap
39	53	7.7	1694	US-10-425-114-12718	Sequence 12718, A
40	53	7.7	2705	US-10-424-599-48931	Sequence 48931, A
41	52.6	7.7	715	US-10-424-599-43172	Sequence 43172, A
42	52.6	7.7	1219	US-10-424-599-130828	Sequence 130828, A
43	52	7.6	1051	US-10-767-701-9350	Sequence 9350, Ap
44	52	7.6	1737	US-09-862-027-13	Sequence 13, Appli
45	52	7.6	1737	US-10-989-228-13	Sequence 13, Appli

## ALIGNMENTS

RESULT 1  
US-10-283-023-1  
; Sequence 1, Application US/10283023  
; Publication No. US20030091573A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: Methods and compositions for the  
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
; FILE REFERENCE: MP01-2391RM  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1705  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-283-023-1

Query Match 100.0%; Score 684; DB 14; Length 1705;  
Best Local Similarity 100.0%; Pred. No. 1.4e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTAGAGCTTCGCGAGTATCCCGTGTGAACCACTTAATTTGTAAGCTTTATGAGCC 60  
DB 226 GTAGAGCTTCGCGAGTATCCCGTGTGAACCACTTAATTTGTAAGCTTTATGAGCC 285

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QY 61 TCGTGAATCCAGTGTCTTGTGATGATAATGCTGAAGGGGCTCTTATATATG 120
DB 286 TCGTGAATCCAGTGTCTTGTGATGATAATGCTGAAGGGGCTCTTATATATG 345
QY 121 CTGCAATGAGTGAACCATTCGCAATTTACTGCTGCCACAGCAATGAGTTGTTTA 180
DB 346 CTGCAATGAGTGAACCATTCGCAATTTACTGCTGCCACAGCAATGAGTTGTTTA 405
QY 181 CAGTGTCCCAAGAGAGTGGCTTATCTTCAACAGATGCAACCAAGGCTAATTCACAG 240
DB 406 CAGTGTCCCAAGAGAGTGGCTTATCTTCAACAGATGCAACCAAGGCTAATTCACAG 465
QY 241 GACCTGAACCAACCAACTTACTGCTGGTTGCAAGGGGGAAGTCTTAAAAATTTGAT 300
DB 466 GACCTGAACCAACCAACTTACTGCTGGTTGCAAGGGGGAAGTCTTAAAAATTTGAT 525
QY 301 TTTGTGACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGGCTTGG 360
DB 526 TTTGTGACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGGCTTGG 585
QY 361 ATGGCACTGAAGTTTGAAGATGATTAATTAACAGTGAAGAAATGACGTTCAGCTGG 420
DB 586 ATGGCACTGAAGTTTGAAGATGATTAATTAACAGTGAAGAAATGACGTTCAGCTGG 645
QY 421 GGTATTATTCTTTGGGAAGTATACGGGTGGAAACCTTTGATGATGATTTGGGCCCA 480
DB 646 GGTATTATTCTTTGGGAAGTATACGGGTGGAAACCTTTGATGATGATTTGGGCCCA 705
QY 481 GCTTTCGAATCATGTGGGCTGTTCAATATGATCTGACACACATGATTAATAATTTA 540
DB 706 GCTTTCGAATCATGTGGGCTGTTCAATATGATCTGACACACATGATTAATAATTTA 765
QY 541 CCTAAGCCATTGAGAGCTGATGATCTGTTGTTGTTTAAAGATCCTTCCAGGCGCT 600
DB 766 CCTAAGCCATTGAGAGCTGATGATCTGTTGTTGTTTAAAGATCCTTCCAGGCGCT 825
QY 601 TCAATGAGGAATTTGAAATTAATGATCACTTGAAGGGATCTTCCAGAGAGAT 660
DB 826 TCAATGAGGAATTTGAAATTAATGATCACTTGAAGGGATCTTCCAGAGAGAT 885
QY 661 GAGCATTACAGTATCCTTGTGAG 684
DB 886 GAGCATTACAGTATCCTTGTGAG 909
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RESULT 2
US-10-283-023-3
; Sequence 3, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using
; FILE REFERENCE: MP101-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1557)
US-10-283-023-3
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Query Match 100.0%; Score 684; DB 14; Length 1705;  
Best Local Similarity 100.0%; Pred. No. 1,4e-207;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 226 GTAGAGCTTGGCAATTATCCGTGTGAACCAATCCTAATATGTAAAGCTTATGAGCC 285
QY 61 TCGTGAATCCAGTGTCTTGTGATGATAATGCTGAAGGGGCTCTTATATATG 120
DB 286 TCGTGAATCCAGTGTCTTGTGATGATAATGCTGAAGGGGCTCTTATATATG 345
QY 121 CTGCAATGAGTGAACCATTCGCAATTTACTGCTGCCACAGCAATGAGTTGTTTA 180
DB 346 CTGCAATGAGTGAACCATTCGCAATTTACTGCTGCCACAGCAATGAGTTGTTTA 405
QY 181 CAGTGTCCCAAGAGAGTGGCTTATCTTCAACAGATGCAACCAAGGCTAATTCACAG 240
DB 406 CAGTGTCCCAAGAGAGTGGCTTATCTTCAACAGATGCAACCAAGGCTAATTCACAG 465
QY 241 GACCTGAACCAACCAACTTACTGCTGGTTGCAAGGGGGAAGTCTTAAAAATTTGAT 300
DB 466 GACCTGAACCAACCAACTTACTGCTGGTTGCAAGGGGGAAGTCTTAAAAATTTGAT 525
QY 301 TTTGTGACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGGCTTGG 360
DB 526 TTTGTGACAGCTGTGACATTCAGACACACATGACCAATTAACAGGGGAGTGGCTTGG 585
QY 361 ATGGCACTGAAGTTTGAAGATGATTAATTAACAGTGAAGAAATGACGTTCAGCTGG 420
DB 586 ATGGCACTGAAGTTTGAAGATGATTAATTAACAGTGAAGAAATGACGTTCAGCTGG 645
QY 421 GGTATTATTCTTTGGGAAGTATACGGGTGGAAACCTTTGATGATGATTTGGGCCCA 480
DB 646 GGTATTATTCTTTGGGAAGTATACGGGTGGAAACCTTTGATGATGATTTGGGCCCA 705
QY 481 GCTTTCGAATCATGTGGGCTGTTCAATATGATCTGACACACATGATTAATAATTTA 540
DB 706 GCTTTCGAATCATGTGGGCTGTTCAATATGATCTGACACACATGATTAATAATTTA 765
QY 541 CCTAAGCCATTGAGAGCTGATGATCTGTTGTTGTTTAAAGATCCTTCCAGGCGCT 600
DB 766 CCTAAGCCATTGAGAGCTGATGATCTGTTGTTGTTTAAAGATCCTTCCAGGCGCT 825
QY 601 TCAATGAGGAATTTGAAATTAATGATCACTTGAAGGGATCTTCCAGAGAGAT 660
DB 826 TCAATGAGGAATTTGAAATTAATGATCACTTGAAGGGATCTTCCAGAGAGAT 885
QY 661 GAGCATTACAGTATCCTTGTGAG 684
DB 886 GAGCATTACAGTATCCTTGTGAG 909
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RESULT 3
US-10-386-414-12
; Sequence 12, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
; APPLICANT: Rodison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: MP103-0210NMIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
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PRIOR APPLICATION NUMBER: 09/330,970  
 PRIOR FILING DATE: 1999-06-11  
 PRIOR APPLICATION NUMBER: 09/724,599  
 PRIOR FILING DATE: 2000-11-28  
 PRIOR APPLICATION NUMBER: 09/860,193  
 PRIOR FILING DATE: 2001-05-16  
 PRIOR APPLICATION NUMBER: 10/283,023  
 PRIOR FILING DATE: 2002-10-29  
 PRIOR APPLICATION NUMBER: 60/335,044  
 PRIOR FILING DATE: 2001-10-31  
 PRIOR APPLICATION NUMBER: 10/010,943  
 PRIOR FILING DATE: 2001-12-06  
 PRIOR APPLICATION NUMBER: 60/254,037  
 PRIOR FILING DATE: 2000-12-07  
 PRIOR APPLICATION NUMBER: 09/833,082  
 PRIOR FILING DATE: 2001-04-10  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 12  
 LENGTH: 1705  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-386-414-12

Query Match 100.0%; Score 684; DB 17; Length 1705;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-207;  
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGACC 60  
 226 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGACC 285  
 61 TGTGTAATCCAGTGTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATG 120  
 286 TGTGTAATCCAGTGTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATG 345  
 121 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
 346 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 405  
 181 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 406 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 465  
 241 GACCTGAACCAACCAACTTACTGCTGTGATGATGATGATGATGATGATGATGATGATG 300  
 466 GACCTGAACCAACCAACTTACTGCTGTGATGATGATGATGATGATGATGATGATGATG 525  
 301 TTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 526 TTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 585  
 361 ATGGACCTGAAGTTTGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 586 ATGGACCTGAAGTTTGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 645  
 421 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 480  
 646 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 705  
 481 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 540  
 706 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 765  
 541 CCTAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
 766 CCTAGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825  
 601 TCAATGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 826 TCAATGAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 885  
 661 GAGCCATTACAGTATCTTGTGAG 684

Db 886 GAGCCATTACAGTATCTTGTGAG 909

RESULT 4  
 US-10-158-895-14  
 Sequence 14, Application US/10158895  
 Publication No. US20020155624A1  
 GENERAL INFORMATION:  
 APPLICANT: ONO, KOICHIRO  
 APPLICANT: OHTOMO, TOSHIHIRO  
 APPLICANT: TSUCHIYA, MASAYUKI  
 TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
 FILE REFERENCE: 053466/0278  
 CURRENT APPLICATION NUMBER: US/10/158,895  
 PRIOR APPLICATION NUMBER: US/09/529,279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 14  
 LENGTH: 1788  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7)...(1776)  
 US-10-158-895-14

Query Match 100.0%; Score 684; DB 13; Length 1788;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-207;  
 Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGACC 60  
 232 GTAGAGCTTGGGAGGATATCCCGTGTGAACCATCTTAATATTTGTAAGCTTTATGAGACC 291  
 61 TGTGTAATCCAGTGTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATG 120  
 292 TGTGTAATCCAGTGTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATG 351  
 121 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
 352 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411  
 181 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 412 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 471  
 241 GACCTGAACCAACCAACTTACTGCTGTGATGATGATGATGATGATGATGATGATGATG 300  
 472 GACCTGAACCAACCAACTTACTGCTGTGATGATGATGATGATGATGATGATGATGATG 531  
 301 TTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
 532 TTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591  
 361 ATGGACCTGAAGTTTGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 592 ATGGACCTGAAGTTTGAAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 651  
 421 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 480  
 652 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 711  
 481 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 540  
 712 GGTATTAATCTTTGGGAAGTATTAACGGCTCGAACCCTTTGATGATGATGATGATGATG 771

QY 54 CTTAAGGCCATTAGAGCCGTGAAGATCGTGTGTGTCTAAAGATCCCTCCCAAGGCCCT 600  
Db 772 CTTAAGGCCATTAGAGCCGTGAAGATCGTGTGTGTCTAAAGATCCCTCCCAAGGCCCT 831  
QY 601 TCAATGAGAGGAATTTGTGAAATTAAGAATCACTGAATGCGGACTTTCCAGAGCGAAT 660  
Db 832 TCAATGAGAGGAATTTGTGAAATTAAGAATCACTGAATGCGGACTTTCCAGAGCGAAT 891  
QY 661 GAGCCATTACAGTAATCCTTGCAG 684  
Db 892 GAGCCATTACAGTAATCCTTGCAG 915

## RESULT 5

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? Sequence 14, Application US/10384743
? Publication No. US20030162228A1
? GENERAL INFORMATION:
? APPLICANT: ONO, KOICHIRO
? APPLICANT: OHTOMO, TOSHIHIRO
? APPLICANT: TSUCHIYA, MASAYUKI
? TITLE OF INVENTION: METHOD OF SCREENING TGF- $\beta$  INHIBITORY SUBSTANCES
? FILE REFERENCE: 053466/0278
? CURRENT APPLICATION NUMBER: US/10/384,743
? CURRENT FILING DATE: 2003-03-11
? PRIOR APPLICATION NUMBER: US/09/529,279
? PRIOR FILING DATE: 2000-04-11
? PRIOR APPLICATION NUMBER: PCT/J998/04796
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: JP 9/290188
? PRIOR FILING DATE: 1997-10-22
? NUMBER OF SEQ ID NOS: 48
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 14
? LENGTH: 1788
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (7)..(1776)
?-S-10-384-743-14

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Query Match	100.0%;	Score 684;	DB 16;	Length 1788;
Best Local Similarity	100.0%;	Pred. No. 1.4e-207;		
Matches 684;	Conservative 0;	Mismatches 0;	Indels 0;	

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTAAAGCTTCGGCAGTATATCCGTTGGAAACATCCCAATATATGTAAACCTTTATGAGCC	60
Db	232	GTAAAGCTTCGGCAGTATATCCGTTGGAAACATCCCAATATATGTAAACCTTTATGAGCC	291
QY	61	TGCTTGAATCAGTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATGTG	120
Db	292	TGCTTGAATCAGTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATGTG	351
QY	121	CTGATAGTGCTGAACCATTTGCCATTTTAACTGCTGCCACGCAATGAGTTGTGTTTA	180
Db	352	CTGATAGTGCTGAACCATTTGCCATTTTAACTGCTGCCACGCAATGAGTTGTGTTTA	411
QY	181	CAGTGTTCCCAAGAGTGCTTATCTTGAACACATGCAACCCAAAGGCTTAATTCACAG	240
Db	412	CAGTGTTCCCAAGAGTGCTTATCTTGAACACATGCAACCCAAAGGCTTAATTCACAG	471
QY	241	GACCTGAACCAACCAACTTACTGCTGTGTGACGGGGGAGCAGTTCTTAAAAATTGTAT	300
Db	472	GACCTGAACCAACCAACTTACTGCTGTGTGACGGGGGAGCAGTTCTTAAAAATTGTAT	531
QY	301	TTTGTGTAACGCTGTGACATTCAGACACACATGACCAATTAACAAGGGAGTGCTGTGG	360
Db	532	TTTGTGTAACGCTGTGACATTCAGACACACATGACCAATTAACAAGGGAGTGCTGTGG	591
QY	361	ATGGCACTGAAGTTTTTGAAGGTGATTAACGTGAAAAATGTGACGTCTTCAAGTGG	420
Db	592	ATGGCACTGAAGTTTTTGAAGGTGATTAACGTGAAAAATGTGACGTCTTCAAGTGG	651

QY 421 GGATTAATTCCTTTGGGAAAGTGAATAACGGGTGGAAAACCTTTTANTGAGATTGGTGCCCA 480

Db 652 GGATTAATTCCTTTGGGAAAGTGAATAACGGGTGGAAAACCTTTTANTGAGATTGGTGCCCA 711

QY 481 GCCTTTCGAAATCATGTGGGCTCTTTCAATAATGTACTGACACACACTGATPAAAAATTTA 540

Db 712 GCCTTTCGAAATCATGTGGGCTCTTTCAATAATGTACTGACACACACTGATPAAAAATTTA 771

QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGGTGTCTAAAGATCCTTCCAGCGCCCT 600

Db 772 CCTAAGCCCATTTGAGAGCCTGATGACTGTTGGTGTCTAAAGATCCTTCCAGCGCCCT 831

QY 601 TCATATGAGAAATTTGTGAAAATAATGACTCACTTGAATGCGGTACTTTCCAGAGCAGAT 660

Db 832 TCATATGAGAAATTTGTGAAAATAATGACTCACTTGAATGCGGTACTTTCCAGAGCAGAT 891

QY 661 GAGCCATTACAGATCCTTGTACG 684

Db 892 GAGCCATTACAGATCCTTGTACG 915

## RESULT 6

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/ Sequence 3, Application US/10158895
/ Publication No. US20020155624M1
/ GENERAL INFORMATION:
/ APPLICANT: ONO, KOICHIRO
/ APPLICANT: OHTOMO, TOSHIHIKO
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
/ FILE REFERENCE: 053466/0278
/ CURRENT APPLICATION NUMBER: US/10/158, 895
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/529, 279
/ PRIOR FILING DATE: 2000-04-11
/ PRIOR APPLICATION NUMBER: PCT/JP98/04796
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: JP 9/290188
/ PRIOR FILING DATE: 1997-10-22
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2656
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (183)..(1919)
/ OS-10-158-895-3

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Query Match	100.0%;	Score 684;	DB 13;	Length 2656;
Best Local Similarity	100.0%;	Pred. No. 1.7e+207;		
Matches 684;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	GTGACCTTGGGAGATTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGACC	60
Db	408	GTGAGAGCTTGGGAGATTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGACC	467
Oy	61	TGCTTAATCCAGTGTGTCTTGTAATGGAATAATGCTGAGGGGGCTCTTAATATAATGTG	120
Db	468	TGCTTAATCCAGTGTGTCTTGTAATGGAATAATGCTGAGGGGGCTCTTAATATAATGTG	527
Oy	121	CTGCATGTGTCTGAACCATTTGCCATATTAATACTGTGCCAGCGCAATAGATGTGTGTTTA	180
Db	528	CTGCATGTGTCTGAACCATTTGCCATATTAATACTGTGCCAGCGCAATAGATGTGTGTTTA	587
Oy	181	CAGTGTGCCAAGGAGTGGCTTAATCTTACACGACATGCAACCGAAGGGCTAATTCACAGG	240
Db	588	CAGTGTGCCAAGGAGTGGCTTAATCTTACACGACATGCAACCGAAGGGCTAATTCACAGG	647
Oy	241	GACCTGAACCAACCAACTTACTGTGTGTGACAGGGGGACAGTTCTAAATAATTTGTGAT	300



Db	648	GACCTGAACAACCAACCAACTACTGCTGTTGACAGGGGGGACAGTTCTAAAAATTGTGAT	707
Qy	301	TTTGTACAGCCTGTGACATTACAGACACATGACCAATPAACAAGGGAGTGTGCTTGG	360
Db	708	TTTGTGACAGCCTGTGACATTACAGACACATGACCAATPAACAAGGGAGTGTGCTTGG	767
Qy	361	ATGGCACTGAAGTTTGAAGGTGATATTACAGTGAATAATGTGACGTCTTCACTGG	420
Db	768	ATGGCACTGAAGTTTGAAGGTGATATTACAGTGAATAATGTGACGTCTTCACTGG	827
Qy	421	GGTATATTCTTTTGGGAAGTGATPAACGGCGTGGAAACCTTTGATGAAATTGGTGGCCA	480
Db	828	GGTATATTCTTTTGGGAAGTGATPAACGGCGTGGAAACCTTTGATGAAATTGGTGGCCA	887
Qy	481	GCTTTCGGAATCATGTGGGCTGTTCATATATGTACTGACCAACAACCTGATTAATAATTTA	540
Db	888	GCTTTCGGAATCATGTGGGCTGTTCATATGTACTGACCAACAACCTGATTAATAATTTA	947
Qy	541	CCTAAGCCCATTTGAGAGCCTGATGCTGTTGGTCTAAAGATCCTTCCAGAGCCCT	600
Db	948	CCTAAGCCCATTTGAGAGCCTGATGCTGTTGGTCTAAAGATCCTTCCAGAGCCCT	1007
Qy	601	TCAATGAGAGAAATTGTGAAAAATATGACTCACTGATGCGGTACTTCCAGAGACAGAT	660
Db	1008	TCAATGAGAGAAATTGTGAAAAATATGACTCACTGATGCGGTACTTCCAGAGACAGAT	1067
Qy	661	GAGCATTACAGTATCCTTGTCAAG	684
Db	1068	GAGCATTACAGTATCCTTGTCAAG	1091

```

RESULT 7
US-10-384-743-3
; Sequence 3, Application US/10384743
; Publication No. US2003016228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04736
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/250188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)..(1919)
US-10-384-743-3

```

Query Match	100.0%	Score 684:	DB 16,	Length 2656;
Best Local Similarity	100.0%	Pred. NO. 1.7e-207;		
Matches 684; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 GRGAGAGCTTGCGCAGTTATCCGCTGGAAACATCCAAATTTTGAAGCTTATGAGGC 60  
Db 408 GTAGAGCTTCGGCAGTTATCCCGTGGAAACATCCAAATTTTGAAGCTTATGAGGC 467  
QY 61 TCGTTGAATCCCAATGTGTCTTGTGAAGAAATAGCTGAAGGGGGCTTTATATATATG 120  
Db 468 TCGTTGAATCCCAATGTGTCTTGTGAAGAAATAGCTGAAGGGGGCTTTATATATATG 527  
QY 121 CTGACATGCTGGAACCAATGGCCATATATADACTGCTGCCACGCAATGATGGTGTGTTA 180

Db	528	CTGCATGCTGTGTAACCATTCGCATATTATATACGTCTGCCACGGAATGAGTGGTGTTA	587
Qy	181	CAGTGTTCACAGGAGTGGCTTATCTTCAACAGATGCACACCCAAGGCTTATTCACAGG	240
Db	588	CAGTGTTCACAGGAGTGGCTTATCTTCAACAGATGCACACCCAAGGCTTATTCACAGG	647
Qy	241	GACCTGAACCAACCAACTTACTGCTGTGGCAGGGGGGACGTTCTTAAAAATTGGAT	300
Db	648	GACCTGAACCAACCAACTTACTGCTGTGGCAGGGGGGACGTTCTTAAAAATTGGAT	707
Qy	301	TTTGGTACGCTGTGACATTCAACAACAATGACCAATTAACAAGGGGAGTGTCTGG	360
Db	708	TTTGGTACGCTGTGACATTCAACAACAATGACCAATTAACAAGGGGAGTGTCTGG	767
Qy	361	ATGGCACTGAAGTTTTTGAAGTAGTATTAACAGTGAATAAATGTGACGTCTTCAGCTGG	420
Db	768	ATGGCACTGAAGTTTTTGAAGTAGTATTAACAGTGAATAAATGTGACGTCTTCAGCTGG	827
Qy	421	GGTATTATCTTTGGGAGATGATACCGGCTGGAAACCTTTGATGAGATTGTGGCCCA	480
Db	828	GGTATTATCTTTGGGAGATGATACCGGCTGGAAACCTTTGATGAGATTGTGGCCCA	887
Qy	481	GCTTTCGGAATCATGTGGGCTGTTCAATATGTAATCTGACCAACACTGATTAATAATTTA	540
Db	888	GCTTTCGGAATCATGTGGGCTGTTCAATATGTAATCTGACCAACACTGATTAATAATTTA	947
Qy	541	CCTTAAGCCCATTTGAGAGCTGTATGACTGTGTGGTTAAAGATCCTTCCACGCGCCT	600
Db	948	CCTTAAGCCCATTTGAGAGCTGTATGACTGTGTGGTTAAAGATCCTTCCACGCGCCT	1007
Qy	601	TCAATGAGGAAATTGTGAAAAATATGACTCACTTGATGCGGTACTTCCAGGAGCAGAT	660
Db	1008	TCAATGAGGAAATTGTGAAAAATATGACTCACTTGATGCGGTACTTCCAGGAGCAGAT	1067
Qy	661	GAGGCATTACAGTATCCTGTGAG	684
Db	1068	GAGGCATTACAGTATCCTGTGAG	1091

```

RESULT 8
US-10-343-710-107
; Sequence 107, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: METZELS, Ingrid
; APPLICANT: WENNDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M., K.-H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343,710
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 107
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-343-710-107

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	Query Match	Best Local Similarity	100.0%;	Score 684;	DB 18;	length 2769;
	Matches	684;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
QY	1	GTAGAGCTTCGGCAGATTACCGTGTGAAACCATCTTAATTGTGAACTTATGAGACC	60			
Db	388	GTAGAGCTTCGGCAGATTACCGTGTGAAACCATCTTAATTGTGAACTTATGAGACC	447			
QY	61	TGCTTGAAATCCAGTGTGTCTTGATGAAATATGCTGAAGGGGGCTCTTATATATATG	120			

Db	448	TGCTTGAATCCAGTGTGTCTTGTAAGAAATAGCTGAAGGGGCTCTTTATATATATG	507
OY	121	CTGCATGCGCTGGAACCATTCGCAATTTATATACCTGCTGGCCAGCGAATGAGTGGTCTTA	180
Db	508	CTGCATGCGCTGGAACCATTCGCAATTTATATACCTGCTGGCCAGCAATGAGTGGTCTTA	567
OY	181	CAGTGTCCCAAGAGGTGGCTTATCTTCAACAGATGCCAACCGGCTAAATTCAAGG	240
Db	568	CAGTGTCCCAAGAGGTGGCTTATCTTCAACAGATGCCAACCGGCTAAATTCAAGG	627
OY	241	GACCTGAAACCAACCAACTTACCTGCTGGTTCAGAGGGGGACGTTCTAAAAATTTGTAT	300
Db	628	GACCTGAAACCAACCAACTTACCTGCTGGTTCAGAGGGGGACGTTCTAAAAATTTGTAT	687
OY	301	TTTGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG	360
Db	688	TTTGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTCTGCTGG	747
OY	361	ATGGACCTGGAAGTTTGAAGGTAGTAATTCACTGAAAAATGTGACGTCTTCAGCTGG	420
Db	748	ATGGACCTGGAAGTTTGAAGGTAGTAATTCACTGAAAAATGTGACGTCTTCAGCTGG	807
OY	421	GGATATATCTTTTGGGAAGTATAACGGTCGGAACCTTGATGAGATTGGTGGCCCA	480
Db	808	GGATATATCTTTTGGGAAGTATAACGGTCGGAACCTTGATGAGATTGGTGGCCCA	867
OY	481	GCTTTCGCAATCATGTGGGCTGTTCAATATGTGACTGCACCACTGATATAAAAATTTA	540
Db	868	GCTTTCGCAATCATGTGGGCTGTTCAATATGTGACTGCACCACTGATATAAAAATTTA	927
OY	541	CCTAAGCCCATGTAGAGCCTGATGACTGGTTGGTAAAGATCCTTCCAGGCGCT	600
Db	928	CCTAAGCCCATGTAGAGCCTGATGACTGGTTGGTAAAGATCCTTCCAGGCGCT	987
OY	601	TCAATGAGGAAATTTGAAAAATATGACTCACTTGATGCGGTACTTTCCAGAGACAGAT	660
Db	988	TCAATGAGGAAATTTGAAAAATATGACTCACTTGATGCGGTACTTTCCAGAGACAGAT	1047
OY	661	GAGCCATTACAGTATCCCTGTACG	684
Db	1048	GAGCCATTACAGTATCCCTGTACG	1071

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RESULT 9
US-09-938-842A-882
; Sequence 882: Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-882

```

	Matches	171;	Conservative	0;	Mismatches	176;	Indels	0;	Gaps	0;
QY	338	ATTAACAAGGGAGT	GTGCTGCTTGAT	TGACACCTGAAGTTTGAAGT	AGTATATTCAGTG	397				
Db	956	ATTAACATAGGA	CTTATAGGTGAT	TGGACCTGAAGTTTAAACCGAT	TACACATGGAC	1015				
QY	358	AAAAATGACGT	CTTCAGCTGGGGT	ATATTTCTTTGGAA	GTGATAACGGT	CGGAAC	457			
Db	1016	GGAAGTGGGA	GGTTTATATGTTTGGAC	TTCTTTATGGGAAT	TGGTAGCTGGACAC	CTTC	1075			
QY	458	CTTTGATGAGAT	TGGTGCGCCAG	CTTTCGAAATCAT	GTGGGCTGTTCAT	ATATGTTACT	517			
Db	1076	CATATGAGGAAT	GAAATTTGCTGTA	CAAAATGCTTACGCA	GTATATATCAAGAA	AAATTA	1135			
QY	518	GACCAACCACT	GATATAAAATTTTAC	CTTAAGCCATTGAG	CGCTGATGACTGTTGGT	577				
Db	1136	GGCCAGTTAT	ACGACCGGATTTGTC	ACAGGGCCATGAA	AGAGCTATCGAGG	ATGTTGGT	1195			
QY	578	CTAAAGATC	CTTCCAGCGCCCTTCA	ATGAGGAATTTG	AAAAATATATGAC	TCACTGTA	637			
Db	1196	CATGCGAAAC	GAGACAAAGACCGGA	ATTTGCGCAGATTTG	CTCAAGTGTGGAA	CATTTC	1255			
QY	638	TGCGTACTTT	CCAGAGCAGAT	TAGGCATTAC	AGTATCTTGT	CAG	684			
Db	1256	AGAACTCT	TACAGCGAAGGAA	AACTTATATCTTT	TACCTAGG	CCAG	1302			

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RESULT 10
US-09-938-842A-882
; Sequence 882, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 882
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-882

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	Query Match	9.6%	Score 65.4	DB 11	Length 1428
	Best Local Similarity	49.3%	Pred. No. 1	Id. No. 1	
	Matches 171	Conservative 0	Mismatches 176	Indels 0	Gaps 0
QY	338	ATTAACAAAGGGAGAGCTCTTGATGCGACCTGAAAGTTTGAAGGTAAATTAACAAGT	397		
Db	956	ATTAACATAGAAACTTAATAGGTGATGAGCAGCTGAAGTTTAAAGGATACCAATGAGAC	1015		
QY	398	AAAAATGTAGAGCTCTTACAGCTGGGGGTATATCTTTGGGAAGATGAATAACGGCTCGAAGAC	457		
Db	1016	GGAAGTGGAGATTATAGCTTTTGAGACTTCTTTATAGGAAATAGTAGCTGAGACATTC	1075		
QY	458	CTTTGATGAGATTGTGGCCCAAGCTTTCGATCATGTGGCTGTTCAATATGATCTC	517		
Db	1076	CATATGAGGAGATGAATTTGCTGAACTAATGCTTACGAGATTATATACAAGAAATTA	1135		
QY	518	GACCAACCACTGATTAATAAATTTTACCTTAACCCATTTAGAGCCTGATGACTGTTGTGGT	577		
Db	1136	GCCAGATTATACCGACGAGATTGTCCAGCGCCCATGAAGAAGCTGATTCGAGGAGATTGGT	1195		

QY 578 CTAAGATCTCTCCAGCGCCCTTCATGAGGAATTTGAAATTAAGACTCACTGA 637  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 93253  
; LENGTH: 1733  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(1733)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91656C.1  
US-10-437-963-93253

## RESULT 11

US-10-425-115-92866  
; Sequence 92866, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 92866  
; LENGTH: 2022  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_184684C.1  
US-10-425-115-92866

Query Match 9.4%; Score 64.4; DB 20; Length 2022;  
Best Local Similarity 50.5%; Pred. No. 2.6e-09;  
Matches 211; Conservative 0; Mismatches 201; Indels 6; Gaps 2;

QY 209 ACAGCATGCAACCAAGCGCTTAATTCAGAGGACCTGAAACCAACTTACTGCTGG 268  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 93253  
; LENGTH: 1733  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(1733)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91656C.1  
US-10-437-963-93253

US-10-437-963-93253  
; Sequence 93253, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.

US-10-437-963-93253  
; Sequence 93253, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 93253  
; LENGTH: 1733  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(1733)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91656C.1  
US-10-437-963-93253

Query Match 8.9%; Score 61; DB 19; Length 1733;  
Best Local Similarity 52.9%; Pred. No. 3e-08;  
Matches 155; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 331 ATGACCAATACAGAGGAGTGTCTTGATGACCTGAAGTTTGAAGTAGTAAT 390  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 93253  
; LENGTH: 1733  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; NAME/KEY: unsure  
; LOCATION: (1)..(1733)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_91656C.1  
US-10-437-963-93253

US-09-732-627A-4894  
; Sequence 4894, Application US/09732627A  
; Publication No. US20040123338A1  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(51770)B  
; CURRENT APPLICATION NUMBER: US/09/732,627A  
; CURRENT FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 4930  
; SEQ ID NO 4894  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3493-039-P1-M1-E4  
US-09-732-627A-4894

US-09-732-627A-4894  
; Sequence 4894, Application US/09732627A  
; Publication No. US20040123338A1  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(51770)B  
; CURRENT APPLICATION NUMBER: US/09/732,627A  
; CURRENT FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 4930  
; SEQ ID NO 4894  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3493-039-P1-M1-E4  
US-09-732-627A-4894

Query Match 8.3%; Score 56.8; DB 11; Length 476;  
Best Local Similarity 53.4%; Pred. No. 3.4e-07;  
Matches 143; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

QY 206 TTCAAGCATGTCAACCCAAAGCGCTTAATTCAAGGGACCTGAAACCAACCAACTTACAGC 265

Db 206 TGCATACCTTATTTACAGGAATACCTTCAAGGATCTCAAAATCAAGAAATTTTACTCC 265

QY 266 TGGTTTCAGGGGGGACAGTTCTTAAAAAATTTGATTTTGGATTCAGACCTGTGACATTCAGA 325

Db 266 TTGAGAAAGATATATGTGTGGAAGGTGGACGATTTTGGATTTTCATGCTTAGAATCTCAGT 325

QY 326 CACACATGACCAA---TAAACAAGGGAGGCGCTTGATATGGCACCTGAAGTTTGTGAAG 382

Db 326 GTGGTAGTGCAGAAAGGATTTACAGGTACTTATCGGTGGATGGCACTGAATGAATTAAG 385

QY 383 GTAGTAAATTACAAGTAAAAATGTGACGCTTTCAGCTGGGGATTAATTTCTTTGGGAAGTGA 442

Db 386 AGAAACATCATACAAAGAAAGATGATGTTTACAGTTTTGGCATTAATCTTTGGGAGCTTT 445

QY 443 TAACCGGTGGAAACCCCTTGTATGAT 470

Db 446 TAAAGGCTTTGACCACTTTGCAACAT 473

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RESULT 14
US-09-938-842A-633
; Sequence 633. Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 633
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-633

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Query Match	8.3%	Score 56.6	DB 9	Length 1398
Best Local Similarity	52.3%	Pred. No. 6.9e-07		
Matches 150; Conservative	0	Mismatches 134	Indels 3	Gaps 1

Qy	186	TTCCCAAGAGTGGCTTATCTTCACAGCATGCAACCCAAAGGGCTAATTCACAGAGACT	245
Db	714	TGCAGAAATGCTCTCGAGTTTCCCATCTCCATGAGAAAGCATATGCAACAAGTCT	773
Qy	246	GAACACCAAACTTACTGCTGGTTGCAGGGGGACAG---TCTAAATAATTTGTGATTT	302
Db	774	GAACCCGAAAATATCTCATGTAATACAGATGGCAGCTGATGCTAACAGATTTTGGTTT	833
Qy	303	TGCTACAGCTGTCGATTCAGACACATGACCAATTAACAAAGGAGTGTGTTGGAT	362
Db	834	AGCAAGAGATTTGAAAGAAACACAAAGATCAAACTCCATGTCGGAACCTAGGGAGTAT	893
Qy	363	GGCACTGAAGTTTTTGAAGGTAGTAATTACAGTGAATAAATGTGACGCTTCAGCTGGG	422
Db	894	GGCACTGAAATTTGTCGAGAAAGACATGATTAACACACTGACTGTGGAGCGTAGG	953
Qy	423	TATTATCTTTGGGAAGGATTAACCGCTCGAAACCTTTGATGAGA	469
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RESULT 15
US-09-938-842A-633
; Sequence 633. Application US/09938842A
; Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 633
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-633

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Db	714	TGAGAAATCGTCTTCGAGTTTCCCATCTTCAGAGAAAGGCAATATCACAGAGATTT	773		
QY	246	GAACCAACCAAACTTACTGCTGTGTGACGGGGGACAG--TTCTAAATTAATTGATTT	302		
Db	774	GAACCCCAAAACATACTCATGATACAGATGCGACGATGATCTAACGATTTTGCTTT	833		
QY	303	TGGTCAGCGGTGCATTCGACACACATGACCATTAACAGGGAGTGTGCTTGGAT	362		
Db	834	AGCAAAAGATTTTGAGAAAACACAAAGATCAACTCCATGTGCGAACTACGAGATATAT	893		
QY	363	GGACCTGAAGTTTGAAGGTAGTAATTAACGTGAAAATGTGACGCTTCAGCTGGGG	422		
Db	894	GGACCTGAATTTGTCAGAGAAAAGACATGATTAAGCAGCTGACTGGTGAGCGTAGG	953		
QY	423	TTTATATCTTTGGGAGTGATTAAGCGCGTGAAGACCTTGAATGAA	469		
Db	954	GATTTCTTCGTATGATGCTCACAGAAAGCCAGCTTTTCTGGGA	1000		

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Job time : 735.527 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: August 2, 2005, 17:28:02 ; Search time 22.3378 Seconds

(without alignments)  
4571.612 Million cell updates/sec

Title: US-09-830-144-1\_COPY\_408\_1091

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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6: /cgm2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1252	100.0	579	US-10-158-895-4	Sequence 4, Appli
3	1252	100.0	590	US-09-529-279-15	Sequence 15, Appli
4	1252	100.0	590	US-10-158-895-15	Sequence 15, Appli
5	1252	100.0	633	US-09-949-016-9902	Sequence 9902, Ap
6	392.5	31.3	663	US-09-949-016-7198	Sequence 7198, Ap
7	371	29.6	455	US-09-221-235-5	Sequence 5, Appli
8	371	29.6	455	US-09-221-928-5	Sequence 5, Appli
9	371	29.6	455	US-09-221-527-5	Sequence 5, Appli
10	371	29.6	455	US-09-221-236-5	Sequence 5, Appli
11	371	29.6	455	US-09-221-416-5	Sequence 5, Appli
12	371	29.6	455	US-09-221-245-5	Sequence 5, Appli

13	371	29.6	455	3	US-09-163-115-5	Sequence 5, Appli
14	371	29.6	455	3	US-09-221-528-5	Sequence 5, Appli
15	371	29.6	455	3	US-09-593-553-5	Sequence 5, Appli
16	371	29.6	455	3	US-09-221-237-5	Sequence 5, Appli
17	371	29.6	455	4	US-09-399-588-2	Sequence 2, Appli
18	371	29.6	455	4	US-09-757-982-5	Sequence 5, Appli
19	363.5	29.0	394	4	US-09-345-4735-19	Sequence 19, Appli
20	355	28.4	1036	4	US-10-014-882-2	Sequence 2, Appli
21	355	28.4	1036	4	US-10-419-279-2	Sequence 2, Appli
22	353.5	28.2	668	1	US-08-205-018-2	Sequence 2, Appli
23	353.5	28.2	859	1	US-08-395-580-2	Sequence 2, Appli
24	353.5	28.2	859	1	PCT-US95-02792-2	Sequence 7798, Ap
25	353.5	28.2	891	4	US-09-949-016-7798	Sequence 11735, A
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27	346	27.6	328	4	US-09-345-4738-18	Sequence 8, Appli
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29	345.5	27.6	885	4	US-09-949-016-7769	Sequence 7789, Ap
30	338.5	27.0	835	3	US-09-291-839-2	Sequence 2, Appli
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37	323	25.8	821	1	US-08-003-311B-2	Sequence 2, Appli
38	323	25.8	821	1	US-08-261-432-2	Sequence 2, Appli
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40	320	25.6	253	3	US-09-035-706-5	Sequence 5, Appli
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43	320	25.6	253	3	US-09-566-906-5	Sequence 5, Appli
44	320	25.6	253	4	US-09-589-034-5	Sequence 5, Appli
45	313.5	25.0	850	4	US-09-904-389-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-09-529-279-4  
Sequence 4, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529, 279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-4

Alignment Scores:  
Pred. No.: 2.36e-144  
Score: 1252.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Gaps: 0

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Db      96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
QY      121 CTGCATGGTGTGAAACCATTCGATATTAATCTGCTGCCAAGCAATGATGGTGTTA 180
Db      116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY      181 CAGTGTCCCAAGAGTGGCTTATCTTCAACAGACATGCAACCAAGCCCTAATTCACAG 240
Db      136 GluCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY      241 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGAGAGATTCTAAAATTTGTGAT 300
Db      156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY      301 TTGGTACAGCTGTGACATTCACACACATGACCAATTAACAAGGGAGTGTCTGG 360
Db      176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY      361 ATGGACCTGAAGTTTGAAGTAGTAAATTAATTAACAGTGAATAAATGACGTTCAGCTG 420
Db      196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
QY      421 GGTATTAATCTTTGGGAAGTATTAACCGCTGGAAACCCCTTGAATGATGGTGCCCA 480
Db      216 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
QY      481 GCTTTCGAATCATGTGGGCTGTTCATTAATGTGCTGACCAACCAACGATTAATAATTTA 540
Db      236 AlaPheArgIleMetTyrPheAlaValHisAsnGlyThrArgProLeuIleLysAsnLeu 255
QY      541 CCTAAGCCCATTTGAGAGCTGTGATGCTGTGTGTGTTAAAGATCCCTCCAGCCGCT 600
Db      256 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY      601 TCAATGAGGAATAATTGAAATAATGACTCACTGATGAGGATCTTTCCAGAGCAGAT 660
Db      276 SerMetGluGluIleValIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY      661 GAGCCATTACAGTATCCTTGTCTAG 684
Db      296 GluProLeuGlnTyrProCysGln 303

RESULT 2
US-10-158-895-4
/ Sequence 4, Application US/10158895
/ Patent No. 6551840
/ GENERAL INFORMATION:
/ APPLICANT: ONO, KOICHIRO
/ APPLICANT: OHTOMO, TOSHIHIKO
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
/ FILE REFERENCE: 053466/0278
/ CURRENT APPLICATION NUMBER: US/10/158,895
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US/09/529,279
/ PRIOR FILING DATE: 2000-04-11
/ PRIOR APPLICATION NUMBER: PCT/JP98/04796
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: JP 9/290188
/ PRIOR FILING DATE: 1997-10-22
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 579
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-158-895-4
Alignment Scores:

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Pred. No.: 2,36e-144 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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QY      61 TCGTTGAATCCAGTGTGCTTGTGATGAAATATGCTGAAGGGGGCTTTTATATATG 120
Db      96 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 115
QY      121 CTGCATGGTGTGAAACCATTCGATATTAATCTGCTGCCAAGCAATGATGGTGTTA 180
Db      116 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY      181 CAGTGTCCCAAGAGTGGCTTATCTTCAACAGACATGCAACCAAGCCCTAATTCACAG 240
Db      136 GluCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 155
QY      241 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGAGAGATTCTAAAATTTGTGAT 300
Db      156 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 175
QY      301 TTGGTACAGCTGTGACATTCACACACATGACCAATTAACAAGGGAGTGTCTGG 360
Db      176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY      361 ATGGACCTGAAGTTTGAAGTAGTAAATTAATTAACAGTGAATAAATGACGTTCAGCTG 420
Db      196 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 215
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Db      216 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 235
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QY      541 CCTAAGCCCATTTGAGAGCTGTGATGCTGTGTGTGTTAAAGATCCCTCCAGCCGCT 600
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Db      276 SerMetGluGluIleValIleValIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY      661 GAGCCATTACAGTATCCTTGTCTAG 684
Db      296 GluProLeuGlnTyrProCysGln 303

RESULT 3
US-09-529-279-15
/ Sequence 15, Application US/09529279
/ Patent No. 6451617
/ GENERAL INFORMATION:
/ APPLICANT: ONO, KOICHIRO
/ APPLICANT: OHTOMO, TOSHIHIKO
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
/ FILE REFERENCE: 053466/0278
/ CURRENT APPLICATION NUMBER: US/09/529,279
/ PRIOR FILING DATE: 2000-04-11
/ PRIOR APPLICATION NUMBER: PCT/JP98/04796
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: JP 9/290188
/ PRIOR FILING DATE: 1997-10-22

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NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-15

## Alignment Scores:

Pred. No.:	2,39e-144	Length:	590
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

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QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGGCTTGG 360
DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaIleTrp 195
QY 361 ATGCACCTGGAAGTTTGAAGTAGTAATTAATTAAGTGAATGACGTTTCAAGCTGG 420
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QY 481 GCTTTCGGAATCATGTGGGCTGTTCAATATGTAATGTAATGACCAACCACTGATTAATA 540
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QY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTTGTTTAAAGATCCTTCCAGGCGCCT 600
DB 256 ProLysProIleGlnSerLeuMetThrArgCysTrpSerIlyAspProSerGlnArgPro 275
QY 601 TCAATGAGAGAAATTTGAAAATAATAGTCACTGATGAGCGTACTTTCCAGAGCAAT 660
DB 276 SerMetGlnGlnIleValIysIleMetThrHisLeuMetCysArgTyPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCCTTGTCAAG 684
DB 296 GluProLeuGlnIlyProCysGln 303
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RESULT 4  
US-10-158-895-15  
Sequence 15, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO

APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-15

## Alignment Scores:

Pred. No.:	2,39e-144	Length:	590
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-158-895-15 (1-590)

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QY 61 TGCTTGAATCCAGTGTGCTTGTGATGGAATATGCTGAAGGGGCTCTTTATATATG 120
DB 96 CysLeuAsnProValCysLeuValMetGluTyThrAlaGluGlyGlySerLeuTyAsnVal 115
QY 121 CTGCATGCTGTGCAACATTCGCAATTTATATCTGCTGCCACGCAATGATGTTGTTT 180
DB 116 LeuHisGlyAlaGlnProLeuProTyThrAlaAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGGTTCCTCCAGAGAGTGGCTTATCTTACAGCATGCAACCAAGGCTTAATTCACAG 240
DB 136 GlnCysSerGlnGlyValAlaIleTyLeuHisSerMetGlnProIlySalAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACCAACTTACTGCTGCTGTCAGAGGGGACAGTTCTTAAATTTGAT 300
DB 156 AspLeuLysProProAsnLeuLeuValAlaGlyIleThrValIleuLysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGGCTTGG 360
DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaIleTrp 195
QY 361 ATGCACCTGGAAGTTTGAAGTAGTAATTAAGTGAATTAAGTGAATGACGTTTCAAGCTGG 420
DB 196 MetIleProGlnValIlePheGlnGlySerAsnTyIleSerGlnLysCysAspValPheSerTrp 215
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QY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTTGTTTAAAGATCCTTCCAGGCGCCT 600
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DB 276 SerMetGlnGlnIleValIysIleMetThrHisLeuMetCysArgTyPheProGlyAlaAsp 295
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Db 236 GlnProLeuGlnTyProCysGln 303
RESULT 5
US-09-949-016-9902
/ Sequence 9902, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9902
/ LENGTH: 633
/ TYPE: PRF
/ ORGANISM: Human
US-09-949-016-9902

Alignment Scores:
Pred. No.: 2,47e-144 Length: 633
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-949-016-9902 (1-633)

QY 1 GTGAGCTTGGGAGGATATCCCGTGAACCACTTAAATTTGTAAGCTTTATGAGCC 60
Db 130 ValGlnLeuArgGlnLeuSerArgValAsnHisProAsnHisLeuValHisLeuTyrGlyAla 149
QY 61 TGCTTGATCCAGTGTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 150 CysLeuAsnProValCysLeuValMetGlnTyrHisGlnTyrHisLeuTyrAsnVal 169
QY 121 CTGCATGTGCTGACCACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 170 LeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 189
QY 181 CAGTGTTCACAGAGTGTGCTTATCTTCACAGATGACCAACCAACGCTTATTCACAG 240
Db 190 GlnCysSerGlnGlyAlaAlaTyrLeuHisSerMetGlnProValAlaLeuHisAsp 209
QY 241 GACCTGAAACCAACCACTTACTGCTGTGTCAGAGGGGAGCAAGTTCTAATAATTTGTGAT 300
Db 210 AspLeuHisProProAsnLeuLeuValAlaGlyGlyThrValLeuHisLeuCysAsp 229
QY 301 TTGTGATGAGCCGTGACATTCAGACACATGACCAATTAACAGGGGAGTGTGCTG 360
Db 230 PheGlyThrAlaCysAspHisGlnThrHisMetThrAsnAsnHisGlySerAlaAlaTyr 249
QY 361 ATGGACCTGAAGTTTGAAGTAGTAAATTAACAGTGAATAATGACCTTTCAGCTGG 420
Db 250 MetAlaProGlnValPheGlnGlySerAsnTyrSerGlnTyrCysAspValPheSerTyr 269
QY 421 GGAATATCTTTGGGAAGTGAATGATGAGCGTGGAAACCTTTGATGAGATGTTGTGCCCA 480
Db 270 GlyLeuLeuLeuTyrGlnValHisLeuThrArgArgGlySerProPheAspGlnHisGlyPro 289
QY 481 GCTTCCGATCATGTGGGCTGTTCAATATGATGATGATGATGATGATGATGATGATGAT 540
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Db 290 AlaPheArgHisLeuThrAlaValHisAsnGlyThrArgProProLeuHisLeuAsnLeu 309
QY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Db 310 ProlAspProHisGlnLeuSerLeuMetThrArgCysTyrSerHisAspProSerGlnArgPro 329
QY 601 TCAATGAGAGAAATTTGAAATTAATGATCACTGATGAGGTTACTTTCAGAGACAT 660
Db 330 SerMetGlnGlnTyrValHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeu 349
QY 661 GAGCATTACAGATCTTGTGAG 684
Db 350 GlnProLeuGlnTyProCysGln 357
RESULT 6
US-09-949-016-7198
/ Sequence 7198, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7198
/ LENGTH: 663
/ TYPE: PRF
/ ORGANISM: Human
US-09-949-016-7198

Alignment Scores:
Pred. No.: 6,38e-39 Length: 663
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
Gaps: 6
DB: 4

US-09-830-144-1_COPY_408_1091 (1-684) x US-09-949-016-7198 (1-663)

QY 4 GAGCTTGGGAGGATATCCCGTGAACCACTTAAATTTGTAAGCTTTATGAGCCTGC 63
Db 198 GlnAlaArgLeuPheGlyAlaLeuGlnHisProAsnHisLeuAlaLeuArgGlyAlaCys 217
QY 64 TTGAATCCAAAA--GTGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 117
Db 218 LeuAsnProProHisLeuCysLeuValMetGlnTyrHisArgGlyAlaLeuSerArg 237
QY 118 GTGCTGATGTGCTGACCACTTATGATGATGATGATGATGATGATGATGATGATGATGAT 177
Db 238 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnThrAla 253
QY 178 TTACAGTGTTCACAGAGTGTGCTTATCTTCACAGATGACCAACCAACGCTTATTCACAG 237
Db 254 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProHisLeuHis 273
QY 238 AGGACCTGAACCAACCACTTACTGCTGTT-----GCAGGG 276
Db 274 ArgAspLeuHisSerHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeu 293
QY 277 GGAACATTTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
Db 294 AspThrValLeuHisLeuThrHisPheGlyLeuAlaArgGlnTyrHisLeuThrThrHis 313
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OY      ACCATAACAGGGGGGCTGCTGGTAGATGCGACCTGAACTTTTGAAGTAGTAATTC 333
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      334 MetSerAlaAlGlyInHrTyralatrrpMetAlaPrGluValIleargLeuSerLeuphe 3333
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      334 AGTGAAMAATGTGACCTCTTCACCTGGGTATTATCTTTGGAGAGTGAATACGCGTCGG 453
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      334 SerLybSerSerAspAlTrpSerPheGlyValleuLeuThrGlnleuLeuThrGlyglu 355
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      454 AAACCTTTGATGAGATTGGTGCCCAAGCTTTCCGAATCATGTGGGCTGT---CATAA 510
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      354 ValProTyraArgGluIle-----AspAlaLeuAlaValAlaTyrglyValAlaMetAsn 377
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      511 GGTACTCCGACCACTGATTAATAAAATTTACCTTAAGCCCATGTGAGACCTGATGATCGT 570
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      372 LysLeuThrLeuProIleProSerThrCysPrgIuProheAlaargLeuLeuGlu 397
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      571 TGTGGTCTAAAGATCCTTCGCCGCGCCCTTCATGAGGAAATGTGAAT 621
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY      392 CysTrpAspProAspProHnIsglyArgProAspPheGlySerIleuLys 408
Db      : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

RESULT 7
; US-09-221-235-5
; Sequence 5, Application us/09221235
; Patent No. 6043040
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,235
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-221-235-5

```

[illegible]

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Oy      346  GGAAGTGGCTTTGATATGGCACTGAAGTTTAAAGGTAGTAATTAAGCAAAAAATGT 405
Db      168  G|Th|Th|Phe|Pro|Trp|Met|Ala|Pro|Glu|Val|I|e|G|In|Ser|Leu|Pro|Val|Ser|G|Th|Cys 187
Oy      406  GAGCTCTTCAGCTGGGGGTATTAATCTTTGGGAAAGTAAAGCGCTCGGAAACCCTTGAT 465
Db      188  Asp|Thr|Tyr|Ser|Tyr|G|L|Val|Val|Leu|Trp|G|Met|Leu|Thr|Arg|G|L|Val|Pro|Phe|Lys 207
Oy      466  GAGATTGGTGGCCCAAGCTTTCGAAATCATGTGG--GCTGTTCATATGATGACTCGACA 522
Db      208  G|L|Leu|G|L|u|G|L|y-----Leu|G|I|n|V|a|L|a|T|P|L|e|u|V|a|L|G|I|u|L|y|A|S|n|G|L|u|A|Arg|Leu 225
Oy      523  CCACGTGATAAAAAATTACCTTAAGCCCAATGAGACCCGTGAGACCTCGTGTGGCTTAAA 582
Db      226  Th|I|L|P|r|o|S|e|r|e|T|y|r|P|r|o|A|l|g|e|r|S|p|e|r|h|e|a|L|g|I|u|L|e|u|H|I|S|G|I|n|C|y|r|T|P|L|u|A|L 245
Oy      583  GATCTCTTCAGCGCCCTTCATATGGAGGAAATTTGAAATAATGATG 627
Db      246  Asp|Ala|L|y|L|e|u|A|l|y|A|r|g|P|r|o|S|e|r|P|h|e|L|y|S|G|I|n|L|e|I|e|S|e|r|L|e|u 260

RESULT 8
US-09-221-928-5
; Sequence 5, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI -050
; CURRENT APPLICATION NUMBER: US/09/221,928
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE:
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-928-5

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Alignment Scores:
Pred. No.: 2.3e-36      Length: 455
Score: 371.00      Matches: 81
Percent Similarity: 56.28%      Conservative: 40
Best Local Similarity: 37.67%      Mismatches: 80
Query Match: 29.63%      Indels: 14
DB: 3      Gaps: 8

US-09-830-144-1 COPY 408_1091 (1-684) x US-09-221-928-5 (1-455)

QY 4 GAGCTTCGGCAGTTATCCCGTGTGACACCATCTAAATTGTAAAGCTTATGAGCGCTGC 63
    ||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 53 GUAAGAGUlleuSerValleuSerHlsAgaenllelelglmheyriglyValle 72
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 64 TTGAATCCA-----GTGTGCTTGTGATGATAATGCTGAAGGGGCTTTATTAAT 117
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 73 leugluProfaenlyrclyleValThrngluTyralaSerleuNylgerleuTyraSp 92
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 118 GTGCTGCAGTGT-----GCTGAACCATTTGCATTTATACGTCTGCCACGCAATGAGT 171
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 93 TyrlleAenSerAmaArgserIugluMet-----AspMetAspHsllleMetThr 109
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 172 TGTGTTTAAAGTGTTCCTCCAAAGAGGTGCTTATCTTCAACAGCATGCAACCAAGGCTA 231
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 110 TTralathrAepValAlaIeysIlymethsTyrlleHlImecIulaIaProValysVal 129
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 232 ATTCAAGAGGACCTGAACAACCAAACTTACGTCTGTGTGCAAGGGGGACAGTTCTAAA 251
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 130 lleHlsArgAspIeuNylserAArgAenVallleAlaIaAspIly---ValleuNyls 148
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 252 ATTGTGATTTGTGTAAGCGCTGTGATTCATTGAGACACATGACCAATTAACAAG----- 345
    ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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Dh 149 ILeCyAspPheGly---AlaSerArgPheHisAsnHisThrThiHisMetSerLeuVal 167
Qy 346 GGAAGTCTGCTTGGATGACCTGAAGTTTGGAGGAGTAAATTAAGTGAAGAAAATGT 405
Db 168 GylThrPheProThrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy 406 GACGCTCAGCTGGGGGTATTAATCTTGGGAAGTAAAGCCGTCGGAACCCCTTGAT 465
Db 188 AspThrTySerTyrGlyValValLeuThrGluMetLeuThrArgGluValProPheLys 207
Qy 466 GAGATTGTGGCCCAAGCTTTCGAAATCATGTGG---GCTGTTCAATATGTAATCGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluThrLeu 225
Qy 523 CCACGTGATAAAAAATTTCCTTAAGCCCATTAAGACCTGATGACTGCTGTTGGTCTAAA 582
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuHisGlnCysTrpGluAla 245
Qy 583 GATCCTTCCAGCGCCCTTCAATGGAGGAATTTGGAATAATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260
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## RESULT 9

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US-09-221-527-5
/ Sequence 5, Application US/09221527
/ Patent No. 6146832
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: WMI-050
/ CURRENT APPLICATION NUMBER: US/09/221,527
/ EARLIER FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: 09/163,115
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 455
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-09-221-527-5
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Alignment Scores:
Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
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US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-527-5 (1-455)

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Qy 4 GAGCTTCGGCAGTTATCCCGTGAACCAATCCAAATTTGTAAGCTTATGAGCCTGC 63
Db 53 GluAlaGluIleLeuSerValIleuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
Qy 64 TTGAATCCA-----GTGTCTTGTGATGAAATATGCTGAAGGGGGCTTTATATAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy 118 GTGCTGCATGCT-----GCTGAACCATGTGCCATATTAATGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy 172 TGGTGTTTACAGTGTCCCAAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy 232 ATTCAAGGAGACTGAAACCAACCAACTTAAGCTGCTGTTGACGGGGGACAGTTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaLysGly---ValLeuLys 148
Qy 292 ATTGAGATTTTGTGACAGCTGTGACATTCAGACACATGACACATTAACAG----- 345
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Dh 149 ILeCyAspPheGly---AlaSerArgPheHisAsnHisThrThiHisMetSerLeuVal 167
Qy 346 GGAAGTCTGCTTGGATGACCTGAAGTTTGGAGGAGTAAATTAAGTGAAGAAAATGT 405
Db 168 GylThrPheProThrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187
Qy 406 GACGCTCAGCTGGGGGTATTAATCTTGGGAAGTAAAGCCGTCGGAACCCCTTGAT 465
Db 188 AspThrTySerTyrGlyValValLeuThrGluMetLeuThrArgGluValProPheLys 207
Qy 466 GAGATTGTGGCCCAAGCTTTCGAAATCATGTGG---GCTGTTCAATATGTAATCGACCA 522
Db 208 GlyLeuGluGly-----LeuGlnValAlaTrpLeuValValGluLysAsnGluThrLeu 225
Qy 523 CCACGTGATAAAAAATTTCCTTAAGCCCATTAAGACCTGATGACTGCTGTTGGTCTAAA 582
Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuHisGlnCysTrpGluAla 245
Qy 583 GATCCTTCCAGCGCCCTTCAATGGAGGAATTTGGAATAATG 627
Db 246 AspAlaLysLysArgProSerPheLysGlnIleIleSerIleLeu 260
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## RESULT 10

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US-09-221-236-5
/ Sequence 5, Application US/09221236
/ Patent No. 6146841
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: WMI-050
/ CURRENT APPLICATION NUMBER: US/09/221,236
/ EARLIER FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: 09/163,115
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 455
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-09-221-236-5
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Alignment Scores:
Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
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US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-236-5 (1-455)

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Qy 4 GAGCTTCGGCAGTTATCCCGTGAACCAATCCAAATTTGTAAGCTTATGAGCCTGC 63
Db 53 GluAlaGluIleLeuSerValIleuSerHisArgAsnIleIleGlnPheTyrGlyValIle 72
Qy 64 TTGAATCCA-----GTGTCTTGTGATGAAATATGCTGAAGGGGGCTTTATATAT 117
Db 73 LeuGluProProAsnTyrGlyIleValThrGluTyrAlaSerLeuGlySerLeuTyrAsp 92
Qy 118 GTGCTGCATGCT-----GCTGAACCATGTGCCATATTAATGCTGCCACGCAATGAGT 171
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspHisIleMetThr 109
Qy 172 TGGTGTTTACAGTGTCCCAAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCGCTA 231
Db 110 TrpAlaThrAspValAlaLysGlyMetHisTyrLeuHisMetGluAlaProValLysVal 129
Qy 232 ATTCAAGGAGACTGAAACCAACCAACTTAAGCTGCTGTTGACGGGGGACAGTTCTAAA 291
Db 130 IleHisArgAspLeuLysSerArgAsnValIleAlaLysGly---ValLeuLys 148
```

```
QY 292 ATTGATTTGGTACAGCCTGTGACATTGACACACATGACCAATTAACAAG----- 345
DB 149 IIECyAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTGCCTCTTGATGAGCAGCTGAAGTTTGGAGAGTAGTAATTACAGTGAATAAATGT 405
DB 168 G1YThrPheProThrMetAlaProGluVal111LeuSerLeuProValSerGluThrCys 187
QY 406 GAGCTTTGACGCTGGGTATATTCTTTGGAGAGTAGTAACGGCTGGAAACCTTTGAT 465
DB 188 AspThrTySerTyrglyVal1ValLeuThrGluMetLeuThrArgGluVal1ProPheLys 207
QY 466 GAGATTGTGCGCCAGCTTCCGAATCATGTGG---GCTGTGTAATAGTACTGACCA 522
DB 208 GlyLeuGluGly-----LeuGlnValAla1TrpLeuVal1ValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTATTAACCTTAAGCCATTGAGAGCCTGATGACTGCTGTGCTTAA 582
DB 226 Thr1LeuProSerSerCysProArgSerPheAlaGluLeuMetHisGlnCysTrpGluVala 245
QY 583 GATCCTTCCAGCGCCTTTCATAGAGAGAAATTGTGAATAATATG 627
DB 246 AspAlaLysLysArgProSerPheLysGln1LeuSer1Leu 260
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## RESULT 11

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US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Action, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-416-5
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## Alignment Scores:

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Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
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US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-416-5 (1-455)

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QY 4 GAGCTTGGGAGGATTATCCCGTGTGAACCATCTTAATATTGTAAGCTTTATGAGCCTGC 63
DB 53 Glu1aGlu1leuLeuSerVal1leuSerHisArgAsn1le1leGlnPheTyrglyVal1le 72
QY 64 TTGAATCA-----GTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAT 117
DB 73 LeuGluProProAsnTyrgly1leVal1ThrGluTyra1aSerLeuGlySerLeuTyraP 92
QY 118 GTGCTGATGAGT-----GCTGAACCATTGGCATATTACTGTGCCACGAGCAATGAGT 171
DB 93 Tyr1leAsnSerAsnArgSerGluGluMet-----AspMetAspHis1leMetThr 109
QY 172 TGGTGTTTACAGTGTTCACAGAGAGTGGCTTATCTTCACAGATGCAACCCAAAGCGCTA 231
DB 110 TrpAlaThrAspValAla1aLysGlyMetHisTyrlleuHisMetGluAlaProValLysVal 129
QY 232 ATTCAAGAGGAGCTGAACCAACCAAACTTACTGCTGTGTCAGGGGGGACAGTTCTTAA 291
DB 130 IleHisArgAspLeuLysSerArgAsnVal1Val1leAla1aAspGly---ValLeuLys 148
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```
QY 292 ATTGATTTGGTACAGCCTGTGACATTGACACACATGACCAATTAACAAG----- 345
DB 149 IIECyAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167
QY 346 GGGAGTGCCTCTTGATGAGCAGCTGAAGTTTGGAGAGTAGTAATTACAGTGAATAAATGT 405
DB 168 G1YThrPheProThrMetAlaProGluVal111LeuSerLeuProValSerGluThrCys 187
QY 406 GAGCTTTGACGCTGGGTATATTCTTTGGAGAGTAGTAACGGCTGGAAACCTTTGAT 465
DB 188 AspThrTySerTyrglyVal1ValLeuThrGluMetLeuThrArgGluVal1ProPheLys 207
QY 466 GAGATTGTGCGCCAGCTTCCGAATCATGTGG---GCTGTGTAATAGTACTGACCA 522
DB 208 GlyLeuGluGly-----LeuGlnValAla1TrpLeuVal1ValGluLysAsnGluArgLeu 225
QY 523 CCACTGATTAATAAATTATTAACCTTAAGCCATTGAGAGCCTGATGACTGCTGTGCTTAA 582
DB 226 Thr1LeuProSerSerCysProArgSerPheAlaGluLeuMetHisGlnCysTrpGluVala 245
QY 583 GATCCTTCCAGCGCCTTTCATAGAGAGAAATTGTGAATAATATG 627
DB 246 AspAlaLysLysArgProSerPheLysGln1LeuSer1Leu 260
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## RESULT 12

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US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Action, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,245
; CURRENT FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: US 09/163,115
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-245-5
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## Alignment Scores:

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Pred. No.: 2,3e-36 Length: 455
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
Gaps: 8
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US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-245-5 (1-455)

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QY 64 TTGAATCA-----GTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAT 117
DB 73 LeuGluProProAsnTyrgly1leVal1ThrGluTyra1aSerLeuGlySerLeuTyraP 92
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DB 93 Tyr1leAsnSerAsnArgSerGluGluMet-----AspMetAspHis1leMetThr 109
QY 172 TGGTGTTTACAGTGTTCACAGAGAGTGGCTTATCTTCACAGATGCAACCCAAAGCGCTA 231
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QY 232 ATTCAAGAGGAGCTGAACCAACCAAACTTACTGCTGTGTCAGGGGGGACAGTTCTTAA 291
DB 130 IleHisArgAspLeuLysSerArgAsnVal1Val1leAla1aAspGly---ValLeuLys 148
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Db 130 ILeHiaArgAspLeuIysSerArgAsnValIleAlaAlaAspGly---ValLeuIys 148  
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QY 346 GGGAGTGTCTGCTGATGAGCACTGGAAGTTTGAAGTGAAGTAAATTAACGTGAATAAATGT 405  
Db 168 G1yThrPheProThrPheAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GACGTCTTCAAGCTGGGGATTAATCTTTGGAGATGAATACCGCTGGAAACCTTTGAT 465  
Db 188 AspThrIySerTyrG1yValValLeuThrGluMetLeuThrArgGluValProPheIys 207  
QY 466 GAGATTGGTGGCCACCTTCCGATCATGTGG---GCTGTCAATATGTAATCTGACCA 522  
Db 208 G1yLeuGluGly-----LeuGlnValAlaThrLeuValValGluIyAsnGluArgLeu 225  
QY 523 CCACTGATATAAAATTTACTTAAGCCCATTTGAGAGCTGATGACCTCGTTGGTGTAA 582  
Db 226 ThrIleProSerSerCySerProArgSerPheAlaGluLeuH1sGlnCySerTrpGluAla 245  
QY 583 GATCTTCCACAGCGCCCTTCATGAGAGAAATGTGAAATATATG 627  
Db 246 AspAlaIyLysArgProSerPheIyGlnIleIleSerIleLeu 260

## RESULT 13

US-09-163-115-5  
; Sequence 5, Application US/09163115A  
; Patent No. 6183962  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/163,115A  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRN  
; ORGANISM: Homo sapiens  
US-09-163-115-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-163-115-5 (1-455)

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Db 73 LeuGluProProAsnIyrgIyIleValIlnGluIyAlaSerLeuGluIySerLeuIyAsp 92  
QY 118 GTGCTGCATGT-----GCTGAACCATTCGCATATTATATGCTGCCACGCAATGAGT 171  
Db 93 TyrIleAsnSerAsnArgSerGluGluMet-----AspMetAspH1sIleMetThr 109  
QY 172 TGGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTCAAGATGCAACCCAAAGCGTA 231  
Db 110 TrpAlaThrAspValAlaIySglYmeH1sTyrLeuH1sMetGluAlaProValIySVal 129  
QY 232 ATTCAAGGAGACTGAACCAACCACTTACTGCTGTGACAGGGGAGACATTTAA 291  
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QY 292 ATTGGATTGTTGGTACAGCTGTGACATTCAGACACATGACCAATAACAAG----- 345  
Db 149 ILeCyAspPheGly---AlaSerArgPheH1sAsnH1eThrThH1sMetSerLeuVal 167  
QY 346 GGGAGTGTCTGCTGATGAGCACTGGAAGTTTGAAGTGAAGTAAATTAACGTGAATAAATGT 405  
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QY 406 GACGTCTTCAAGCTGGGGATTAATCTTTGGAGATGAATACCGCTGGAAACCTTTGAT 465  
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QY 466 GAGATTGGTGGCCACCTTCCGATCATGTGG---GCTGTCAATATGTAATCTGACCA 522  
Db 208 G1yLeuGluGly-----LeuGlnValAlaThrLeuValValGluIyAsnGluArgLeu 225  
QY 523 CCACTGATATAAAATTTACTTAAGCCCATTTGAGAGCTGATGACCTCGTTGGTGTAA 582  
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QY 583 GATCTTCCACAGCGCCCTTCATGAGAGAAATGTGAAATATATG 627  
Db 246 AspAlaIyLysArgProSerPheIyGlnIleIleSerIleLeu 260

## RESULT 14

US-09-221-528-5  
; Sequence 5, Application US/09221528  
; Patent No. 6190874  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan  
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNI-050  
; CURRENT APPLICATION NUMBER: US/09/221,528  
; EARLIER FILING DATE: 1998-12-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 455  
; TYPE: PRN  
; ORGANISM: Homo sapiens  
US-09-221-528-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-221-528-5 (1-455)

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Db 53 G1uAlaGluIleuSerValIleuSerH1sArgAsnIleIleGlnH1eThrArgIyValIle 72  
QY 64 TTGAATCCA-----GTGTCTTGTGATGAATATGTAAGGGGGCTTTATATAT 117  
Db 73 LeuGluProProAsnIyrgIyIleValIlnGluIyAlaSerLeuGluIySerLeuIyAsp 92  
QY 118 GTGCTGCATGT-----GCTGAACCATTCGCATATTATATGCTGCCACGCAATGAGT 171  
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QY 172 TGGTGTTTACAGTGTCCCAAGAGAGGCTTATCTTCAAGATGCAACCCAAAGCGTA 231  
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QY 232 ATTCAAGGAGACTGAACCAACCACTTACTGCTGTGACAGGGGAGACATTTAA 291

Db 130 ILeHisrAgAspLeuLySerArgAsnValIleAlaIaAspGly---ValLeuLys 148  
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QY 583 GATCCTTCCAGCGCCCTTCAATGAGAGAAATTTGAAATTAATG 627  
Db 246 AspAlaLysIlybArgProSerPheLysGlnIleIleSerIleLeu 260

RESULT 15  
US-09-593-553-5  
Sequence 5, Application US/09593553  
Patent No. 6200770  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan  
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
FILE REFERENCE: NMI-050  
CURRENT APPLICATION NUMBER: US/09/593,553  
CURRENT FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: 09/163,115  
PRIOR FILING DATE: 1998-09-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-593-553-5

Alignment Scores:  
Pred. No.: 2,3e-36 Length: 455  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-09-593-553-5 (1-455)

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QY 232 ATTCAAGGAGCTGTAACCAACCAAACTTAATGCTGCTGTCAGGGGGGACAGTTCTAATA 291

Db 130 ILeHisrAgAspLeuLySerArgAsnValIleAlaIaAspGly---ValLeuLys 148  
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Db 149 IleCysAspPheGly---AlaSerArgPheHisAsnHisThrThrHisMetSerLeuVal 167  
QY 346 GGGAGTGTCTGTGATGACCTGAGATTTTGGAGGTAGTAAATTAACAGTGAATAAATGT 405  
Db 168 GlyThrPheProTyrMetAlaProGluValIleGlnSerLeuProValSerGluThrCys 187  
QY 406 GACGCTCTGACCTGGGATATTATCTTTGGAGATGATTAACGCTGGAAAACCTTTGAT 465  
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QY 466 GAGATTGTGGCCCAAGCTTCCGAATCATGTGG---GCTGTCATTAATGTACTGACCA 522  
Db 208 GlyLeuGluGly-----LeuGlnValAlaThrLeuValValGluLysAsnGluArgLeu 225  
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Db 226 ThrIleProSerSerCysProArgSerPheAlaGluLeuLeuHisGlnCysTrpGluAla 245  
QY 583 GATCCTTCCAGCGCCCTTCAATGAGAGAAATTTGAAATTAATG 627  
Db 246 AspAlaLysIlybArgProSerPheLysGlnIleIleSerIleLeu 260

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Job time : 28.3378 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: August 2, 2005, 19:59:50 ; Search time 84.7297 Seconds

(without alignments)  
6290.398 Million cell updates/sec

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1252	100.0	336	Sequence 135, App
2	1252	100.0	518	Sequence 2, App1
3	1252	100.0	518	Sequence 13, App1
4	1252	100.0	579	Sequence 4, App1
5	1252	100.0	579	Sequence 4, App1
6	1252	100.0	590	Sequence 15, App1
7	1252	100.0	590	Sequence 15, App1
8	1233.5	98.5	623	Sequence 13442, A
9	1221	97.5	616	Sequence 13629, A
10	1215	97.0	615	Sequence 13628, A
11	815	65.1	268	Sequence 13508, A
12	392.5	31.3	330	Sequence 136, App
13	392.5	31.3	953	Sequence 56, App1
14	392.5	31.3	953	Sequence 98, App1
15	392.5	31.3	954	Sequence 97, App1
16	392.5	31.3	954	Sequence 187, App
17	387.5	31.0	940	Sequence 223, App
18	387.5	31.0	1018	Sequence 13436, A
19	379	30.3	422	Sequence 132604, A
20	377	30.1	376	Sequence 173612, A
21	376	30.0	371	Sequence 13608, A
22	374.5	29.9	376	Sequence 271998, A
23	374.5	29.9	2964	Sequence 13552, A
24	373.5	29.8	603	Sequence 156923, A
25	373	29.8	357	Sequence 252964, A
26	373	29.8	415	Sequence 351552, A
27	373	29.8	426	Sequence 60778, A
28	373	29.8	433	Sequence 57936, A
29	372	29.7	289	Sequence 13427, A
30	372	29.7	415	Sequence 135148, A
31	372	29.7	426	Sequence 55173, A
32	372	29.7	426	Sequence 58969, A
33	372	29.7	454	Sequence 13429, A
34	372	29.6	802	Sequence 13428, A
35	371	29.6	312	Sequence 137, App
36	371	29.6	349	Sequence 6345, App
37	371	29.6	417	Sequence 46822, A
38	371	29.6	455	Sequence 5, App1
39	371	29.6	455	Sequence 2477, App
40	371	29.6	455	Sequence 2, App1
41	371	29.6	455	Sequence 837, App
42	371	29.6	473	Sequence 1101, App
43	371	29.6	800	Sequence 66, App1
44	371	29.6	800	Sequence 64, App1
45	371	29.6	800	Sequence 64, App1

## ALIGNMENTS

RESULT 1  
US-10-664-421-135  
Sequence 135, Application US/10664421  
Publication No. US20040142864A1  
GENERAL INFORMATION:  
APPLICANT: BREMER, RYAN  
APPLICANT: IBRAHIM, PRABHA  
APPLICANT: KIMAR, ABHINAV  
APPLICANT: MANDIYAN, VALSAN  
APPLICANT: MILBURN, MICHAEL V.  
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
FILE REFERENCE: 039363/0703  
CURRENT APPLICATION NUMBER: US/10/664,421  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: 60/412,341  
PRIOR FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: 60/411,398  
PRIOR FILING DATE: 2002-09-16  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: PatentIn Ver. 3.2

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/ SEQ ID NO 135
/ LENGTH: 336
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-664-421-135
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## Alignment Scores:

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Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

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RESULT 2
US-10-283-023-2
/ Sequence 2, Application US/10283023
/ Publication No. US20030091573A1
/ GENERAL INFORMATION:
/ APPLICANT: Carroll, Joseph M.
/ TITLE OF INVENTION: Methods and compositions for the
/ diagnosis and treatment of hematological disorders using
/ TITLE OF INVENTION: 16319
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/ FILE REFERENCE: WP101-239P1RM
/ CURRENT APPLICATION NUMBER: US/10/283,023
/ CURRENT FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 60/335,044
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 518
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-283-023-2
```

## Alignment Scores:

Pred. No.:	3, 14e-128	Length:	518
Score:	1252.00	Matches:	228
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-283-023-2 (1-518)

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QY 1 GTAGAGCTTCGGCAGTTATCCCGTGTGAACCATCTTAATTTGTAACCTTTATGAGCC 60
Db ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyGlyAla 95
QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTCTTATATATATG 120
Db CysLeuAsnProValCysLeuValMetGlnIlyrAlaGlnIlyGlySerLeuTyAsnVal 115
QY 121 CTGATGTGTCTGAACCATTCGATATATATCTGCTGCCACGCAATGATGTGTTA 180
Db LeuHisGlyAlaGlnProLeuProIlyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTACAGCATGCAACCAAGGCTAATTCACAG 240
Db GlnCysSerGlnGlyValAlaIlyrLeuHisSerMetGlnProIlyrAlaLeuIleHisArg 155
QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGACAGTTCTTAAATTTGAT 300
Db AspLeuIlyrProProAsnLeuLeuValAlaGlyIlyrThrValIleLeuIlyrCysAsp 175
QY 301 TTTGGTACAGCTGTGATTCAGACACATGACCAATTAACAAGGAGTGTGCTTGG 360
Db PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIlyrGlySerAlaAlaTyr 195
QY 361 ATGGCAGCTGAAGTTTGAAGGTAATTAACGTAAGTGAAGTGAAGTGAAGTGAAGT 420
Db MetAlaProGlnValIlePheGlnIlyrSerAsnIlyrSerIlyrCysAspValPheSerTyr 215
QY 421 GGTATTAATTTTGGGAAGTATACCGCTCGGAAACCTTTGATGATGTGGGCCA 480
Db GlnIlyrLeuIlyrGlnValIleThrArgIlyrProPheAspGlnIleGlyIlyrPro 235
QY 481 GCTTCCGAATCAGTGGGCTGTTCATATGTAATGTAATGTAATGTAATGTAATGTA 540
Db AlaPheArgIleMetThrAlaValHisAsnGlyThrArgProProLeuIleIlyrAsnLeu 255
QY 541 CCTAAGCCATTGAGAGCTGATGACTCGTTGTGTGAAGATCCTTCCAGCGCCCT 600
Db ProIlyrProIleGlnSerLeuMetThrArgCysTyrSerIlyrAspProSerGlnArgPro 275
QY 601 TCAATGAGGAATTTGAAATTAATGACTCACTTATGTCGATCTTCCAGAGAGCAT 660
Db 276 SerMetGlnIlyrIleValIlyrIleMetThrHisLeuMetArgIlyrPheProGlyAlaAsp 295
QY 661 GAGCATTAACAGTATCCTTGTGAG 684
Db 296 GlnProLeuGlnIlyrProCysGln 303
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RESULT 3
US-10-386-414-13
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Sequence 13, Application US/10386414
Publication No. US20040006016A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Meyers, Rachel E.
APPLICANT: MacBetch, Kyle J.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
FILE REFERENCE: MET03-0210NMIM
CURRENT APPLICATION NUMBER: US/10/386,414
PRIORITY FILING DATE: 2003-03-11
PRIORITY APPLICATION NUMBER: 09/426,282
PRIORITY FILING DATE: 1999-10-25
PRIORITY APPLICATION NUMBER: 09/668,266
PRIORITY FILING DATE: 2000-09-22
PRIORITY APPLICATION NUMBER: 09/330,970
PRIORITY FILING DATE: 1999-06-11
PRIORITY APPLICATION NUMBER: 09/724,599
PRIORITY FILING DATE: 2000-11-28
PRIORITY APPLICATION NUMBER: 09/860,193
PRIORITY FILING DATE: 2001-05-16
PRIORITY APPLICATION NUMBER: 10/283,023
PRIORITY FILING DATE: 2002-10-29
PRIORITY APPLICATION NUMBER: 60/335,044
PRIORITY FILING DATE: 2001-10-31
PRIORITY APPLICATION NUMBER: 10/010,943
PRIORITY FILING DATE: 2001-12-06
PRIORITY APPLICATION NUMBER: 60/254,037
PRIORITY FILING DATE: 2000-12-07
PRIORITY APPLICATION NUMBER: 09/833,082
PRIORITY FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapien
US-10-386-414-13

Alignment Scores:
Pred. No.: 3,14e-128 Length: 518
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 15

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-386-414-13 (1-518)
QY 1 GTAGAGCTTGGGAGATTATCCGTTGTGAACCATCTTAATTTATTAAGCTTTATGAGCC 60
DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIySLeuTyrcIyAla 95
QY 61 TGCCTTGAATCCAGAGTGTCTTGTATGATGAATATGCTGAAGGGGCTCTTTATTAATG 120
DB 96 CysLeuAsnProValCysLeuValMetGluTyraGluGlySerLeuTyraAsnVal 115
QY 121 CTGATGTGTGTGAACCATTCATATATATCTGCTGCCAAGCAATGATGTGTGTTA 180
DB 116 LeuHisGlyAlaGluProLeuProTyrrThraAlaHisAlaMetSerTrpCysLeu 135
QY 181 CAGTGTCCCAAGAGTGGCTTATTTTCAACGATGCAACCAAGCGCTTAATTACAGG 240
DB 136 GlnCysSerGlnGlyValAlaIyrrLeuHisSerMetGlnProIyAlaLeuIleHisArg 155
QY 241 GACCGAAGCAACCAACTTCTGCTGTGTGAGGGGGAAGCTTAAATTTGTGAT 300
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DB 156 AspLeuIyProProAsnLeuLeuValAlaGlyGlyThrValLeuIyIleCysAsp 175
QY 301 TTTGTATAGAGCCCTGTGATTCAGACACATGACCAATTAACAGGGAGTGTCTGTGG 360
DB 176 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnHisGlySerAlaIatrp 195
QY 361 ATGGACCTGAACTTTTGAAGTAGTAATTACAGTAAATAATGTAAGCTTTCAGCTGG 420
DB 196 MetAlaProGluValPheGluGlySerAsnTySerGluIyCysAspValPheSerTrp 215
QY 421 GGTATTAATCTTTGGGAAGTGAATGATTAAGCGTCGGAACCCCTTATGATGATGTGGCCCA 480
DB 216 GlyIleIleLeuTrpGluValIleThrArgAlyLysProPheAspGluIleGlyLysPro 235
QY 481 GCTTCCGATCATGTGGGCTGTCATTAATGTATCTGACCAACCATGATTAATAAATTTA 540
DB 236 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProLeuIleIySAsnLeu 255
QY 541 CCTAAGCCCATGAGAGCCGTGATGACTCGTTGTGTCTAAGATCCTTCCAGCGCCCT 600
DB 256 ProIyProIleGluSerLeuMetThrArgCysTrpSerIySAspProSerGlnArgPro 275
QY 601 TCAATGAGGAATTTGTAATAATTAATGATCACTTGAATGCGGTACTTTCCAGAGCAT 660
DB 276 SerMetGluGluIleValIySLeuMetThrHisLeuMetArgTyrrPheProGlyAlaAsp 295
QY 661 GACCGATTAACATATCTTGTCCAG 684
DB 296 GluProLeuGlnIyrrProCysGln 303

RESULT 4
US-10-158-895-4
Sequence 4, Application US/10158895
Publication No. US20020155624A1
GENERAL INFORMATION:
APPLICANT: ONO, KOICHIRO
APPLICANT: OHTOMO, TOSHIHIKO
APPLICANT: TSUCHIYA, MASAYUKI
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
FILE REFERENCE: 053466/0278
CURRENT APPLICATION NUMBER: US/10/158,895
CURRENT FILING DATE: 2002-06-03
PRIORITY APPLICATION NUMBER: US/09/529,279
PRIORITY FILING DATE: 2000-04-11
PRIORITY APPLICATION NUMBER: PCT/JP98/04796
PRIORITY FILING DATE: 1998-10-22
PRIORITY APPLICATION NUMBER: JP 9/290188
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
US-10-158-895-4

Alignment Scores:
Pred. No.: 3,23e-128 Length: 579
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-4 (1-579)
QY 1 GTAGAGCTTGGGAGATTATCCGTTGTGAACCATCTTAATTTATTAAGCTTTATGAGCC 60
DB 76 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIySLeuTyrcIyAla 95
QY 61 TGCCTTGAATCCAGAGTGTCTTGTATGATGAATATGCTGAAGGGGCTCTTTATTAATG 120
DB 96 CysLeuAsnProValCysLeuValMetGluTyraGluGlySerLeuTyraAsnVal 115
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QY 121 CTGCATGCTGCAACCATTCGCTTACTGCTCCACGCAATGAGTGTGTTA 180  
DB 116 LeuHISGLYALAGLIPROLEUPROTYRTHRILALAHLEALMESETRIPCYSALEU 135  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACACATGCAACCCAAAGCCCTTAATTCACAG 240  
DB 136 GlnCYSSERGLNGLYVALALATYRLEUHSERMETGLNPROLYSALALEUILLHISARG 155  
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTGTCAGGGGGAGACGTTCTAAAAATTTGTAT 300  
DB 156 AspleuLYSPROPROASMEUleuValALAGLYGlyTHRValLeuLYSILECYASAP 175  
QY 301 TTGGTACAGCCTGTCAGATTCAGACACATGACCAATTAACAGGGAGTGTGCTTGG 360  
DB 176 PheGLYTHRAlACYSAspRIEGLNTHRHISMETTHRANASNUYSGLYSERALALATRP 195  
QY 361 ATGGACCTGAAAGTTTGAAGGTAGTAATTACAGTGAAGAAATGTCAGCTTCAGCTGG 420  
DB 196 MetAlAPROGLIValPheGLUGLYSERASNTRYSERGLULYSCYASAPVALPHESETRTP 215  
QY 421 GGTATTATCTTTGGGAAGTGAATAACGCGTCGAAAACCTTTGATGAGATTGTGCGCCA 480  
DB 216 GlyIleIleuTRIPGLIValIleTHRARGLYSPROpHeAspGLIleGLYGLYPRO 235  
QY 481 GCTTCCGATCATGTCGGCTGTTCAATATGTTACTGACACACACATGATTAATAATTTA 540  
DB 236 AlaPheARGILEMETTRPAlaValHISASNGLYTHRARGPROpLeuILLelySAsnLeu 255  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTGTGTTGCTTAAGATCCCTCCAGCGCCT 600  
DB 256 ProLYSPROILEGLUSErLeuMetTHRARGYSTRIPserLYSAspPROSErGLINARGPRO 275  
QY 601 TCATGAGAGAAATTTGAAATAATATGACTCACTTGTAGCGGTACTTTCCAGAGCAGAT 660  
DB 276 SerMetGLUGLIleValLYSILEMETTHRHSISleuMetARGTYRPhEPROGLYAlAsp 295  
QY 661 GAGCCATTACAGTATCCCTTGTGAG 684  
DB 296 GluPROleuGLINTRYPROCYSGIN 303

RESULT 5  
US-10-384-743-4  
; Sequence 4, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITIRO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; PRIOR FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-384-743-4

Alignment Scores:  
Pred. No.: 3,23e-128 Length: 579  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0  
US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-384-743-4 (1-579)  
QY 1 GTAAGCTTTGGGAGATTATCCCGTGTGAACCATCTTAATATTGTAAAGCTTTATGAGGCC 60  
DB 76 ValGLIleuARGLINleuSERARGValAMNHISPROASNILEVALYSleuTRYGLYAlA 95  
QY 61 TGCTTGAATTCAGTGTGTCTTGTGATGGAATATGCTGAAAGGGGGCTTTATTAATAATGTG 120  
DB 96 CyLeuASNPROVALCYsLeuValMetGLUTRYAlAGLUGLYGLYserLeuTRYASNVal 115  
QY 121 CTGCATGCTGCAACCATTCGCTTACTGCTCCACGCAATGAGTGTGTTA 180  
DB 116 LeuHISGLYALAGLIPROLEUPROTYRTHRILALAHLEALMESETRIPCYSALEU 135  
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACACATGCAACCCAAAGCCCTTAATTCACAG 240  
DB 136 GlnCYSSERGLNGLYVALALATYRLEUHSERMETGLNPROLYSALALEUILLHISARG 155  
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTGTCAGGGGGAGACGTTCTAAAAATTTGTAT 300  
DB 156 AspleuLYSPROPROASMEUleuValALAGLYGlyTHRValLeuLYSILECYASAP 175  
QY 301 TTGGTACAGCCTGTCAGATTCAGACACATGACCAATTAACAGGGAGTGTGCTTGG 360  
DB 176 PheGLYTHRAlACYSAspRIEGLNTHRHISMETTHRANASNUYSGLYSERALALATRP 195  
QY 361 ATGGACCTGAAAGTTTGAAGGTAGTAATTACAGTGAAGAAATGTCAGCTTCAGCTGG 420  
DB 196 MetAlAPROGLIValPheGLUGLYSERASNTRYSERGLULYSCYASAPVALPHESETRTP 215  
QY 421 GGTATTATCTTTGGGAAGTGAATAACGCGTCGAAAACCTTTGATGAGATTGTGCGCCA 480  
DB 216 GlyIleIleuTRIPGLIValIleTHRARGLYSPROpHeAspGLIleGLYGLYPRO 235  
QY 481 GCTTCCGATCATGTCGGCTGTTCAATATGTTACTGACACACACATGATTAATAATTTA 540  
DB 236 AlaPheARGILEMETTRPAlaValHISASNGLYTHRARGPROpLeuILLelySAsnLeu 255  
QY 541 CCTAAGCCCATTTGAGAGCCTGATGACTGTGTGTTGCTTAAGATCCCTCCAGCGCCT 600  
DB 256 ProLYSPROILEGLUSErLeuMetTHRARGYSTRIPserLYSAspPROSErGLINARGPRO 275  
QY 601 TCATGAGAGAAATTTGAAATAATATGACTCACTTGTAGCGGTACTTTCCAGAGCAGAT 660  
DB 276 SerMetGLUGLIleValLYSILEMETTHRHSISleuMetARGTYRPhEPROGLYAlAsp 295  
QY 661 GAGCCATTACAGTATCCCTTGTGAG 684  
DB 296 GluPROleuGLINTRYPROCYSGIN 303

RESULT 6  
US-10-158-895-15  
; Sequence 15, Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITIRO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15

```

; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-15

Alignment Scores:
Pred. No.: 3,25e-128 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-158-895-15 (1-590)

QY 1 GTAGAGCTTGGGCGAGTTATCCGTTGAGAACCATCTTAATATTGTAAGCTTTATGAGACC 60
DB ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
QY 61 TGCCTTGAATCCAGTGTCTTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
DB CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGAGTGTGTAACCATTCATATATATCTGCTGCCACGCAATGATGCTGTTTA 180
DB LeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAG 240
DB GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTTGACGGGGGACAGTTCTTAAATTTGTAT 300
DB AspLeuAsnProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGATTCACAGACACATGACCAATTAACAAGGGAGTGGCTTGG 360
DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGGCACTGGAAGTTTGAAGGTATTAACAGTGAATAAATGACGCTTTCAGCTGG 420
DB MetAlaProGlnValPheGlnGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 215
QY 421 GGTATTATCTTTGGGAAGTATTAACGGCTGGAAAACCTTTGATGAGATTGGTGCCCA 480
DB GlyIleIleLeuTyrGlnValIleThrArgArgLysProPheAspGlnIleGlyCysPro 235
QY 481 GCTTCCGAATCATGTGGGCTGTTTCATATGCTACGACCAACCACTGATTAATAATTA 540
DB GCTTCCGAATCATGTGGGCTGTTTCATATGCTACGACCAACCACTGATTAATAATTA 540
QY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTGTCTTAAAGATCTTCCAGAGCCCT 600
DB ProlIysProIleGlnSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGAGAAATTTGAAAATAATGACTCACTTGATGCGGTACTTTCCAGAGACAG 660
DB 276 SerMetGlnGlnIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCCTTGTTCAG 684
DB 296 GluProLeuGlnTyrProCysGln 303

RESULT 7
US-10-384-743-15
; Sequence 15, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAHUKU
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
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; CURRENT APPLICATION NUMBER: US/10/384,743
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-743-15

Alignment Scores:
Pred. No.: 3,25e-128 Length: 590
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-384-743-15 (1-590)

QY 1 GTAGAGCTTGGGCGAGTTATCCGTTGAGAACCATCTTAATATTGTAAGCTTTATGAGACC 60
DB ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAla 95
QY 61 TGCCTTGAATCCAGTGTCTTGTGTGATGGAATATGCTGAAGGGGCTCTTTATATATATG 120
DB CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsnVal 115
QY 96 CysLeuAsnProValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsnVal 115
QY 121 CTGATGAGTGTGTAACCATTCATATATATCTGCTGCCACGCAATGATGCTGTTTA 180
DB LeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 135
QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCACAGATGCAACCAAGCGCTAATTCACAG 240
DB GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeuIleHisArg 155
QY 241 GACCTGAAACCAACCAACTTACTGCTGTGTTGACGGGGGACAGTTCTTAAATTTGTAT 300
DB AspLeuAsnProProAsnLeuLeuValAlaGlyGlyThrValLeuIysIleCysAsp 175
QY 301 TTTGGTACAGCTGTGATTCACAGACACATGACCAATTAACAAGGGAGTGGCTTGG 360
DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 195
QY 361 ATGGCACTGGAAGTTTGAAGGTATTAACAGTGAATAAATGACGCTTTCAGCTGG 420
DB MetAlaProGlnValPheGlnGlySerAsnTyrSerGlnLysCysAspValPheSerTyr 215
QY 421 GGTATTATCTTTGGGAAGTATTAACGGCTGGAAAACCTTTGATGAGATTGGTGCCCA 480
DB GlyIleIleLeuTyrGlnValIleThrArgArgLysProPheAspGlnIleGlyCysPro 235
QY 481 GCTTCCGAATCATGTGGGCTGTTTCATATGCTACGACCAACCACTGATTAATAATTA 540
DB GCTTCCGAATCATGTGGGCTGTTTCATATGCTACGACCAACCACTGATTAATAATTA 540
QY 541 CTTAAGCCCATTTGAGAGCTGATGACTGTTGTGTCTTAAAGATCTTCCAGAGCCCT 600
DB ProlIysProIleGlnSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 275
QY 601 TCAATGAGAGAAATTTGAAAATAATGACTCACTTGATGCGGTACTTTCCAGAGACAG 660
DB 276 SerMetGlnGlnIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 295
QY 661 GAGCCATTACAGTATCCTTGTTCAG 684
DB 296 GluProLeuGlnTyrProCysGln 303
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RESULT 8  
 US-10-732-923-13442  
 ; Sequence 13442, Application US/10732923  
 ; Publication No. US20050108791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; PRIOR FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 13442  
 ; LENGTH: 623  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-732-923-13442

Alignment Scores:  
 Pred. No.: 3,566-126 Length: 623  
 Score: 1233.50 Matches: 228  
 Percent Similarity: 93.06% Conservative: 0  
 Best Local Similarity: 93.06% Mismatches: 0  
 Query Match: 98.52% Indels: 17  
 DB: 17 Gaps: 1

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-732-923-13442 (1-623)

QY 1 GTAGAGCTTCGGAGATTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGAGCC 60  
 DB ValGluLeuAArgGlnLeuSerAArgValAsnHisProAsnIleValIlySLeuYrGlyAla 95  
 QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTTTATATATATATG 120  
 DB CysLeuAsnProValCysLeuValMeGluYrAlaGluGlyGlySerLeuYrAsnVal 115  
 QY 121 CTGCATGCTGTGAACCATGTCATATTATATGCTGCTGCCACCGAAGAGTTGGTGT 180  
 DB LeuHisGlyAlaGluProLeuProYrYrThrAlaAlaHisAlaMetSerTrpCysLeu 135  
 QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATTCACAG 240  
 DB GlnCysSerGlnGlyValAlaYrLeuHisSerMetGlnProIlySalLeuIleHisArg 155  
 QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGGCAAGTCTTAATAATTTGTAT 300  
 DB AspLeuAsnProProAsnLeuLeuValAlaGlyGlyThrValLeuYrIleCysAsp 175  
 QY 301 TTGTGTACAGCTGTGATTCATTCAGACACATGACCAATTAAGGGAGTGTGCTGG 360  
 DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnYrGlySerAlaAlaTrp 195  
 QY 361 ATGGCACCCTGAAGTTTGAAGGTAGTAATTAAGTGAATAATGTAGCTTCACCTGG 420  
 DB MetAlaProGluValPheGlnGlySerAsnYrSerGluYrCysAspValPheSerTrp 215  
 QY 421 GGTATTATCTTTGGGGAAGGATTAACGCGTCGGAACCCCTTGAATGAATGGTGGCCCA 480  
 DB GlyIleIleLeuTrpGluValIleThrArgArgValPheProLeuIleYrAsnLeu 235  
 QY 481 GCTTTCGAATCATGTGGGCTGTTCATTAATGTACTGACCAACCATGTAATAAATTGA 540  
 DB AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleYrAsnLeu 255  
 QY 541 CCGAAGCCATTGAGAGCTGATGATCTGTTGTGTCTTAAGATCTTCCAGGGCCCT 600  
 DB ProIlySerProIleGlnSerLeuMetThrArgCysTrpSerIlyAspProSerGlnArgPro 275  
 QY 601 TCAATGAGAAATGTGAAATAATGACTCACTGATGCGG----- 642  
 DB SerMetGluGluIleValIlySerIleMetThrHisLeuMetArgGlyLeuLeuCysThrGlu 295

QY 643 -----TACTTTCAGAGACAGATGAGCCATTA 669  
 DB GlyIleLeuAsnArgAspLeuLeuLeuGlnIlyPheProGlyAlaAspGluProLeu 315  
 QY 670 CAGATCCTTGTGAG 684  
 DB 316 GlnIlyProCysGln 320

RESULT 9  
 US-10-732-923-13629  
 ; Sequence 13629, Application US/10732923  
 ; Publication No. US20050108791A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edgerton, Michael D  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
 ; FILE REFERENCE: 38-15(52796)C  
 ; CURRENT APPLICATION NUMBER: US/10/732,923  
 ; PRIOR FILING DATE: 2003-12-10  
 ; PRIOR APPLICATION NUMBER: 10/310,154  
 ; PRIOR FILING DATE: 2002-12-04  
 ; NUMBER OF SEQ ID NOS: 24149  
 ; SEQ ID NO 13629  
 ; LENGTH: 616  
 ; TYPE: PRT  
 ; ORGANISM: Xenopus laevis  
 US-10-732-923-13629

Alignment Scores:

Pred. No.: 8,396-125 Length: 616  
 Score: 1221.00 Matches: 222  
 Percent Similarity: 98.68% Conservative: 3  
 Best Local Similarity: 97.37% Mismatches: 3  
 Query Match: 97.52% Indels: 0  
 DB: 17 Gaps: 0

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-732-923-13629 (1-616)

QY 1 GTAGAGCTTCGGAGATTATCCGCTGTGAACCATCTTAATATTGTAAGCTTTATGAGCC 60  
 DB ValGluLeuAArgGlnLeuSerAArgValAsnHisProAsnIleValIlySLeuYrGlyAla 84  
 QY 61 TGCCTGAATCCAGTGTCTTGTGATGGAATATGCTGAAGGGGCTTTATATATATG 120  
 DB CysLeuAsnProValCysLeuValMeGluYrAlaGluGlyGlySerLeuYrAsnVal 104  
 QY 121 CTGCATGCTGTGAACCATGTCATATTATATGCTGCTGCCACCGAAGAGTTGGTGT 180  
 DB LeuHisGlyAlaGluProLeuProYrYrThrAlaAlaHisAlaMetSerTrpCysLeu 124  
 QY 181 CAGTGTCCCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGGCTTAATTCACAG 240  
 DB GlnCysAlaGlnGlyValAlaYrLeuHisSerMetIlySerProIlySalLeuIleHisArg 144  
 QY 241 GACCTGAACCAACCAACTTACTGCTGTGTCAGGGGGGCAAGTCTTAATAATTTGTAT 300  
 DB AspLeuAsnProProAsnLeuLeuValAlaGlyGlyThrValLeuYrIleCysAsp 164  
 QY 301 TTGTGTACAGCTGTGATTCATTCAGACACATGACCAATTAAGGGAGTGTGCTGG 360  
 DB PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnYrGlySerAlaAlaTrp 184  
 QY 361 ATGGCACCCTGAAGTTTGAAGGTAGTAATTAAGTGAATAATGTAGCTTCACCTGG 420  
 DB MetAlaProGluValPheGlnGlySerAsnYrSerGluYrCysAspValPheSerTrp 204  
 QY 421 GGTATTATCTTTGGGGAAGGATTAACGCGTCGGAACCCCTTGAATGAATGGTGGCCCA 480  
 DB GlyIleIleLeuTrpGluValIleThrArgArgValPheProLeuIleYrAsnLeu 224  
 QY 481 GCTTTCGAATCATGTGGGCTGTTCATTAATGTACTGACCAACCATGTAATAAATTGA 540  
 DB AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleYrAsnLeu 244

Alignment Scores:	
Pred. No.:	3.83e-124
Score:	1215.00
Percent Similarity:	98.25%
Best Local Similarity:	96.93%
Query Match:	97.04%
DB:	17
US-09-830-144-1_COPY.408.1091 (1-684) x US-10-732-923-13628 (1-615)	
Length:	615
Matches:	221
Conservative:	3
Mismatches:	4
Indels:	0
Gaps:	0

Qy	481	GCCTTCCGAATCAGTGGGGCTGTCATTAATGTAAGTCTGACACACCACTGATTAATAAATTTA	544	50
Db	225	AlaheargilewettrpAlaValhlsansglYthArgProboleuilelyshsnleu	244	
Qy	541	CCTAAGCCCATTTGAGAGCCGTGATGACTGTGTGGTCTTAAGATCCTTCCAGCGCCCT	600	
Db	245	ProlyseProilegluserleuemetthrArgCystrpserlyshAspProProglInArgPro	264	
Qy	601	TCAAATGAGAGAAATTTGAAAAATAATGACTCACTTGAATGCGGTACTTTCCAGAGACAT	660	
Db	265	SermetglugluileVallyleillemetthrhlshleuylsGlnTyPheProglYlaAsp	284	
Qy	661	GAGCCATTACAGTATCTTCTTGAC	684	
Db	285	ValserleuglnTyPProCysglIn	292	
RESULT 11				
US-10-732-923-13508				
; Sequence 13508, Application US/10732923				
; Publication No. US20050108791A1				
; GENERAL INFORMATION:				
; APPLICANT: Edgeton, Michael D				
; TITLE OR INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES				
; FILE REFERENCE: 38-15(52796)C				
; CURRENT APPLICATION NUMBER: US/10/732,923				
; CURRENT FILING DATE: 2003-12-10				
; PRIOR APPLICATION NUMBER: 10/310,154				
; PRIOR FILING DATE: 2002-12-04				
; NUMBER OF SEQ ID NOS: 24149				
; SEQ ID NO 13508				
; LENGTH: 268				
; TYPE: PRT				
; ORGANISM: Anopheles gambiae str. PEST				
US-10-732-923-13508				
Alignment Scores:				
Pred. No.: 2,8e-80 Length: 268				
Score: 815.00 Matches: 151				
Percent Similarity: 77.68% Conservative: 23				
Best Local Similarity: 67.41% Mismatches: 46				
Query Match: 65.10% Indels: 4				
DB: 17 Gaps: 3				
US-09-830-144-1_COPY_408_1091 (1-684) x US-10-732-923-13508 (1-268)				
Qy	4	GAGCTTCGGGCACTTATCCCGTGTGAACCATCTTAATTTGTAAGCTTTATGAGCGCTGC	63	
Db	36	GluValserhlshleuSerArgValAlahlsProAsnlelellegluLeuTyglYlaCys	55	
Qy	64	TTGAATCCA-----GTGTCCTTGATGAGTAATGCGAAGGGGGCTTTATATTAAT	117	
Db	56	ThrGluTyProAsnPhcCylLeuValMetGluTyAlAspLylyleuSerlyshlslys	75	
Qy	118	GTGCTGCAATGCGTGAACCATTTGSCATTTACTGCTGCCACGCCAATGAATGGTGT	177	
Db	76	ValLeuHls--SerArgProArgProValTyThrAlaAlahlsblametsertprala	94	
Qy	178	TTACAGTGTCCCAAGAGATGSCCTTATCTTCAcAGATGCGAACCCAAAGCGCTAATTAC	233	
Db	95	ArgGlnCysAlaGlulglYalaAlaTyglLeuHlsAspMetThrProArgPrometllehis	114	
Qy	238	AGGACCTGAAACCAACCAAACTTACTGCTGCTTGCAAGGGGGGACAGTCTTAATAATTTGT	297	
Db	115	ArgAspLeuTyPProAsnleuLeuValAsnAsnGlyThrValleuLyslleCys	133	
Qy	298	GATTTTGTGATGAGCGCTGTGACATTGACACATGACCAATTAACAAGGAGATGCTGCT	357	
Db	135	AspPheGlyThrValThrAspLysSerThrleuMetThrAsnleuTysglyserAlaala	154	
Qy	358	TGATATGCACTGAATTTTGAAGGTAGTAATTAACGTGAATAATGTGACGTCTTGAC	417	
Db	155	TyrMetAlaProGluValPheGlnGlySerSerTyThrGluTyCysAspValPheSer	174	



## Alignment Scores:

Pred. No.: 1.05e-33 Length: 953  
 Score: 392.50 Matches: 88  
 Percent Similarity: 56.68% Conservative: 35  
 Best Local Similarity: 40.55% Mismatches: 77  
 Query Match: 31.35% Indels: 17  
 DB: 15 Gaps: 6

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-369-022-56 (1-953)

```

QY 4 GAGCTTGGGACGATATCCCGTGAACCATCTTAATTTGTAAGCTTTATGAGCCGTC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GlnAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgGlyAlaCys 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAGATATGCTGAAGGGGCTCTTATATAT 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 LeuAsnProPheHisLeuGlySLeuValMetGlnTyrAlaArgGlyAlaLeuSerArg 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 GTGCTGATGCTGCTGAACCATTCCTATTTATCTGCTGCCACGCAATGAGTTGCTGT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnTyrAla 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 TTACAGTGTCCCAAGAGGTGGCTTATCTTCAAGATGCAACCCAAAGGCTATTCAC 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleIleHis 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 AGGACCTGGAACCAACCACTTACTGCTGCT-----GCAGGG 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 ArgAspLeuLysSerIleAsnIleLeuIleLeuGlnAlaIleGlnAsnHisAsnLeuAla 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GGGACAGTTCTAAAAATTTGTGATTTTGTGACAGCTGTGAC--ATTGACACACATG 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGlnTyrPheIleThrLys 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 334 ACCAAATAACAAGGAGATGCTGCTGATGAGCTGCACTGAAGTTTGAAGTAAATTAAC 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 261 MetSerIleAlaGlyIleThrTyrAlaTyrPheAlaProGlnValIleArgLeuSerLeuPhe 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 AGTGAATAATGTGAGCTGCTGAGTGGGGTATTAATCTTTGGAGATGAACGCTCGG 453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 SerIysSerIleAspValIleTyrSerPheGlyValLeuLeuTyrGlnLeuLeuThrGlyGln 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 AAACCTTTGATGATGATGTTGTGGCCAGCTTTCCGAATCATGTGGCTGTT--CATPAT 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 ValProTyrArgGlnIle-----AspAlaLeuAlaValAlaTyrGlyValAlaMetAsn 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 511 GGTACTGACCAACACATGATATAAAATTTACTTAAGCCCATTTGAGAGCTGATACCTGT 570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 319 LysLeuThrLeuProIleProSerThrCysProGlnProPheAlaArgLeuGlnGln 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 TGTGAGTCTAAAGATCTTCCAGGCGCCCTCAATGAGAGAAATTTGTGAAA 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 CysTyrAspProAspProHisGlyArgProAspPheGlySerIleLeuLys 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

## RESULT 14

US-10-042-865-98  
 Sequence 98, Application US/10042865  
 Publication No. US20040029216A1

## GENERAL INFORMATION:

GENERAL INFORMATION:  
 APPLICANT: Padigar, Muralidhara  
 APPLICANT: Li, Li  
 APPLICANT: Zeehuseen, Bryan D  
 APPLICANT: Casman, Stacie J  
 APPLICANT: Shenoy, Suresh G  
 APPLICANT: Spytek, Kimberly  
 APPLICANT: Zhong, Mei  
 APPLICANT: Gangolli, Esna A  
 APPLICANT: Burgess, Catherine B  
 APPLICANT: Patcurajan, Meera  
 APPLICANT: Verner, Corine A.M  
 APPLICANT: Taylor, Sarah  
 APPLICANT: Tchiernev, Velizar T

```

APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Boldog, Ferenc L
APPLICANT: Grose, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Gerlach, Valerie L
APPLICANT: Edinger, Shlomit R
APPLICANT: Rothenberg, Mark B
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Malyankar, Uriel M
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glenda
APPLICANT: Gunther, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 98
LENGTH: 953
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-865-98
  
```

## Alignment Scores:

Pred. No.: 1.05e-33 Length: 953  
 Score: 392.50 Matches: 88  
 Percent Similarity: 56.68% Conservative: 35  
 Best Local Similarity: 40.55% Mismatches: 77  
 Query Match: 31.35% Indels: 17  
 DB: 15 Gaps: 6

US-09-830-144-1\_COPY\_408\_1091 (1-684) x US-10-042-865-98 (1-953)

```

QY 4 GAGCTTGGGACGATATCCCGTGAACCATCTTAATTTGTAAGCTTTATGAGCCGTC 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GlnAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgGlyAlaCys 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 TTGAATCCA-----GTGTGCTTGTGATGAGATATGCTGAAGGGGCTCTTATATAT 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 LeuAsnProPheHisLeuGlySLeuValMetGlnTyrAlaArgGlyAlaLeuSerArg 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 GTGCTGATGCTGCTGAACCATTCCTATTTATCTGCTGCCACGCAATGAGTTGCTGT 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 185 ValLeuAlaGlyArgValProProHisVal-----LeuValAsnTyrAla 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 TTACAGTGTCCCAAGAGGTGGCTTATCTTCAAGATGCAACCCAAAGGCTATTCAC 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 ValGlnValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProValProIleIleHis 220
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 AGGACCTGGAACCAACCACTTACTGCTGCT-----GCAGGG 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 ArgAspLeuLysSerIleAsnIleLeuIleLeuGlnAlaIleGlnAsnHisAsnLeuAla 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GGGACAGTTCTAAAAATTTGTGATTTTGTGACAGCTGTGAC--ATTGACACACATG 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 AspThrValLeuLysIleThrAspPheGlyLeuAlaArgGlnTyrPheIleThrLys 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

```

QY 334 ACCAATACAGGAGGAGCTGCTGATGATGACCTGAAGTTTGAAGTAGTAATAC 393
Db 261 MetSerAlaIaGlyThrTyraIatrpMetAlaProGluValIlaArgLeuSerIeuPhe 280
QY 394 AGTGAATAATGTGACGCTTCCAGCGGGGTATATTTCTTTGGAGAGTGAATACGGCTCGG 453
Db 281 SerIysSerSerAspValItrpSerPheGlyValIleuLeuItrpGluIleuThrGlyGlu 300
QY 454 AAACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
Db 301 ValProIyArGluIle-----AspAlaIeuaIaValaIaTyGlyValaIaMetAsn 318
QY 511 GGTACTGCACGACCACTGATTAATAAATTACTTAAGCCCATTTGAGACCTGATGACTCGT 570
Db 319 LysIleuThrLeuProIleProSerThrCysProGluItrpPheAlaArgLeuIleuGlu 338
QY 571 TGTGGTCTAAAGATCTTCCAGCGCCCTTCATGATGAGAAATGTGAAA 621
Db 339 CysItrpAspProAspProHisGlyArGpProAspPheGlySerIleIeuIys 355

RESULT 15
US-10-042-865-97
/ Sequence 97, Application US/10042865
/ Publication No. US20040029216A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Li, Li
/ APPLICANT: Zernhusen, Bryan D
/ APPLICANT: Caeman, Stacie J
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zhong, Mei
/ APPLICANT: Gangoli, Bsha A
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Vermet, Corine A.M
/ APPLICANT: Taylor, Sarah
/ APPLICANT: Tcherenev, Velizar T
/ APPLICANT: Miller, Charles E
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Boldog, Ference L
/ APPLICANT: Grose, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Macdougall, John
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Miller, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smitson, Glenda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, David
/ TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
/ TIME OF INVENTION: Using the Same
/ FILE REFERENCE: 21402-537
/ CURRENT APPLICATION NUMBER: US/10/042,865
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/260,417
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/260,831
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/272,338
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/274,876
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/284,704
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 264
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 97
/ LENGTH: 954

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/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-042-865-97

Alignment Scores:
Pred. No.: 1,05e-33
Score: 392.50
Percent Similarity: 56.68%
Best Local Similarity: 40.55%
Query Match: 31.35%
DB: 15
Gaps: 6

US-09-830-144-1_COPY_408_1091 (1-684) x US-10-042-865-97 (1-954)

QY 4 GAGCTTGCGCAGATATCCGCTGAAACCTCTTAATATTGTAAGCTTATGACCTTCG 63
Db 145 GluAlaArgLeuPheGlyValaIeuGlnIAspRoanIleIleAlaIeuArgGlyAlaCys 164
QY 64 TTGAATCCA-----GTGTCTTGATGATGATGATGATGATGATGATGATGATGATGAT 117
Db 165 LeuAsnProProHisIleuIeuCysIleuValIeuGlnIAspRoanIleIleAlaIeuSerArg 184
QY 118 GTGCTGCATGCTGCTGCAACCATTCGATTAATTAATCTGCTGCCACGCAATGATGATGT 177
Db 185 ValIeuAlaGlyArGArGValProProHisVal-----LeuValAsnItrpAla 200
QY 178 TTACAGTGTCCCAAGAGGTGCTTATCTTCAACGATGCAACCCAAAGCCCTTAATTCAC 237
Db 201 ValGlnValAlaArgGlyMetAsnIlyIeuHisAsnAspAlaProValProIleHis 220
QY 238 AGGACCTGAAACCAACCAACTTACTGCTGCT-----GCAAGG 276
Db 221 ArgAspLeuIysSerIleAsnIleuIleuIleuGlnAlaIleuGlnAsnIleuAla 240
QY 277 GGGACAGTCTTAAATTTGATTTGTACAGCTGTAC---ATTGACACACACATG 333
Db 241 AspItrValIeuIysIleThrAspPheGlyIleuAlaArgGlnItrpHisIlySerThrThIys 260
QY 334 ACCAATACAGGAGGAGCTGCTGATGATGACCTGAAGTTTGAAGTAGTAATAC 393
Db 261 MetSerAlaIaGlyThrTyraIatrpMetAlaProGluValIlaArgLeuSerIeuPhe 280
QY 394 AGTGAATAATGTGACGCTTCCAGCGGGGTATATTTCTTTGGAGAGTGAATACGGCTCGG 453
Db 281 SerIysSerSerAspValItrpSerPheGlyValIleuLeuItrpGluIleuThrGlyGlu 300
QY 454 AAACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 510
Db 301 ValProIyArGluIle-----AspAlaIeuaIaValaIaTyGlyValaIaMetAsn 318
QY 511 GGTACTGCACGACCACTGATTAATAAATTACTTAAGCCCATTTGAGACCTGATGACTCGT 570
Db 319 LysIleuThrLeuProIleProSerThrCysProGluItrpPheAlaArgLeuIleuGlu 338
QY 571 TGTGGTCTAAAGATCTTCCAGCGCCCTTCATGATGAGAAATGTGAAA 621
Db 339 CysItrpAspProAspProHisGlyArGpProAspPheGlySerIleIeuIys 355

Search completed: August 2, 2005, 20:33:28
Job time : 90.7297 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 2, 2005, 20:15:38 ; Search time 27.7297 Seconds  
(without alignments)  
613.781 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303

Sequence: 1 VELRQLSRVNHVNIYKLYGA.....MTHLMRYFPQADEPLQYPCQ 228

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiletest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	100.0	579	4	US-09-529-279-4
2	1252	100.0	579	4	US-10-158-895-4
3	1252	100.0	590	4	US-09-529-279-15
4	1252	100.0	590	4	US-10-158-895-15
5	1252	100.0	633	4	US-09-949-016-9902
6	392.5	31.3	663	4	US-09-949-016-7198
7	371	29.6	455	3	US-09-221-235-5
8	371	29.6	455	3	US-09-221-928-5
9	371	29.6	455	3	US-09-221-527-5
10	371	29.6	455	3	US-09-221-236-5
11	371	29.6	455	3	US-09-221-416-5
12	371	29.6	455	3	US-09-221-245-5
13	371	29.6	455	3	US-09-163-115-5
14	371	29.6	455	3	US-09-221-528-5
15	371	29.6	455	3	US-09-593-553-5
16	371	29.6	455	3	US-09-529-237-5
17	371	29.6	455	4	US-09-399-588-2
18	371	29.6	455	4	US-09-757-982-5
19	363.5	29.0	394	4	US-09-345-473E-19
20	363.5	28.4	1036	4	US-10-014-882-2
21	355	28.4	1036	4	US-10-419-279-2
22	353.5	28.2	668	1	US-08-205-018-2
23	353.5	28.2	859	1	US-08-395-580-2
24	353.5	28.2	859	5	PCT-US95-02792-2
25	353.5	28.2	891	4	US-09-949-016-7798
26	352.5	28.2	169	4	US-09-270-767-31735
27	346	27.6	328	4	US-09-345-473E-18

28	345.5	27.6	847	4	US-09-949-016-6222	Sequence 6222, Ap
29	345.5	27.6	885	4	US-09-949-016-7789	Sequence 7789, Ap
30	338.5	27.0	835	3	US-09-291-839-2	Sequence 2, Appli
31	338.5	27.0	835	4	US-09-458-457-2	Sequence 2, Appli
32	338.5	27.0	835	4	US-09-947-199A-2	Sequence 8, Appli
33	335.5	26.8	835	4	US-09-458-457-8	Sequence 8, Appli
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35	331.5	26.5	978	4	US-09-949-016-7281	Sequence 7281, Ap
36	323	25.8	821	1	US-07-928-464-2	Sequence 2, Appli
37	323	25.8	821	1	US-08-003-111B-2	Sequence 2, Appli
38	323	25.8	821	1	US-08-261-432-2	Sequence 2, Appli
39	323	25.8	821	1	PCT-US93-07347-2	Sequence 2, Appli
40	320	25.6	263	3	US-09-035-706-5	Sequence 5, Appli
41	320	25.6	263	3	US-08-955-841-5	Sequence 5, Appli
42	320	25.6	263	3	US-09-390-425-5	Sequence 5, Appli
43	320	25.6	263	3	US-09-566-906-5	Sequence 5, Appli
44	320	25.6	263	4	US-09-589-034-5	Sequence 5, Appli
45	313.5	25.0	850	4	US-09-904-389-2	Sequence 2, Appli

## ALIGNMENTS

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RESULT 1
US-09-529-279-4
; Sequence 4, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIO
; APPLICANT: TSUCHIYA, MAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-4
Query Match 100.0%; Score 1252; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.2e-133;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VELRQLSRVNHVNIYKLYGACINPCLVMEYAEAGSLYVLAHGAELPLPYTAAHMSWCL 60
DB 76 VELRQLSRVNHVNIYKLYGACINPCLVMEYAEAGSLYVLAHGAELPLPYTAAHMSWCL 135
QY 61 QCSQGVATLHSMOPKALIHRLKPNLLVAGTLYKICDGGTACDIDHTMTNKGSAW 120
DB 136 QCSQGVATLHSMOPKALIHRLKPNLLVAGTLYKICDGGTACDIDHTMTNKGSAW 195
QY 121 MAPFVBSGNSSEKCDVFSWGLIIMEVITRRKPPDEIGGAPFRIMWAVHNGTRPPLINL 180
DB 196 MAPFVBSGNSSEKCDVFSWGLIIMEVITRRKPPDEIGGAPFRIMWAVHNGTRPPLINL 255
QY 181 KPPIBSLMTWCMSKDPSPSMETIVKIMTHLMRYFPQADEPLQYPCQ 228
DB 256 KPPIBSLMTWCMSKDPSPSMETIVKIMTHLMRYFPQADEPLQYPCQ 303
RESULT 2
US-10-158-895-4
; Sequence 4, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
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; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-158-895-4
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Query Match      100.0%; Score 1252; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.2e-133;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VELRLSRVNHNPNIYKLYGACINPVCIMVEYAEAGSLYNVLHGAEPPLPYTAAHMSWCL 60
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DB 76 VELRLSRVNHNPNIYKLYGACINPVCIMVEYAEAGSLYNVLHGAEPPLPYTAAHMSWCL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTGACDIQTHMTNKGSAAM 120
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DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTGACDIQTHMTNKGSAAM 195
QY 121 MAPVFEFSNYSSEKCDVFSWGIIIMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180
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DB 196 MAPVFEFSNYSSEKCDVFSWGIIIMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 255
QY 181 PKPIESIMTRCWSKDPSPQSRPSMEIYKIMTHLMRYFPGADEPLQYPCQ 228
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RESULT 3
US-09-529-279-15
; Sequence 15, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-279-15
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Query Match      100.0%; Score 1252; DB 4; Length 590;
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Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTGACDIQTHMTNKGSAAM 120
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DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTGACDIQTHMTNKGSAAM 195
QY 121 MAPVFEFSNYSSEKCDVFSWGIIIMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180
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DB 196 MAPVFEFSNYSSEKCDVFSWGIIIMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 255
QY 181 PKPIESIMTRCWSKDPSPQSRPSMEIYKIMTHLMRYFPGADEPLQYPCQ 228
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DB 256 PKPIESIMTRCWSKDPSPQSRPSMEIYKIMTHLMRYFPGADEPLQYPCQ 303
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RESULT 4
US-10-158-895-15
; Sequence 15, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-158-895-15
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Query Match      100.0%; Score 1252; DB 4; Length 590;
Best Local Similarity 100.0%; Pred. No. 5.3e-133;
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RESULT 5
US-09-949-016-9902
; Sequence 9902, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMOPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 9902  
;; LENGTH: 633  
;; TYPE: PRF  
;; ORGANISM: Human  
US-09-949-016-9902

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Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMSCL 60  
DB 130 VELRQLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMSCL 189

QY 61 QCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKI CDPTACDIQTHMTNKGSAW 120  
DB 190 QCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKI CDPTACDIQTHMTNKGSAW 249

QY 121 MAPVFGSNYSKCDVPSWGIIMVEVITRRKPFDEIGPAPFRIMAVHNGTRPPLIKNL 180  
DB 250 MAPVFGSNYSKCDVPSWGIIMVEVITRRKPFDEIGPAPFRIMAVHNGTRPPLIKNL 309

QY 181 PKPESLMTRCWSKDPSPSMEEIVKIMTAMRYFPDADPLQYPCQ 228  
DB 310 PKPESLMTRCWSKDPSPSMEEIVKIMTAMRYFPDADPLQYPCQ 357

RESULT 6  
US-09-949-016-7198  
;; Sequence 7198, Application US/09949016  
;; Patent No. 6812339  
;; GENERAL INFORMATION:  
;; APPLICANT: VENTER, J. Craig et al.  
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
;; FILE REFERENCE: C0001307  
;; CURRENT APPLICATION NUMBER: US/09/949,016  
;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 7198  
;; LENGTH: 663  
;; TYPE: PRF  
;; ORGANISM: Human  
US-09-949-016-7198

Query Match 31.3%; Score 392.5; DB 4; Length 663;  
Best Local Similarity 40.6%; Pred. No. 1.7e-35;  
Matches 88; Conservative 35; Mismatches 77; Indels 17; Gaps 6;

QY 2 ELRLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMSCL 59  
DB 198 EARLFGALQHPRIITLRGACLNPPHCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMSCL 253

QY 60 LQCSGQVAYLHSMQPKALIHRLDKPNNLLV-----AGTIVLKI CDPTACDIQTHMTNKGSAW 111  
DB 254 VQVAGMYLHNDADVPPIIHRDLKSNILITLAIENHNLTADVTILKITFGLAREWHKXTYK 313

QY 112 TNNKSAAMMAPEVEGNSYSEKCDVPSWGIIMVEVITRRKPFDEIGPAPFRIMAV-HN 170

DB 314 MSAAGTYAMAPREVILSLFSSKSDVMSFGVLLMELLTGBVPYREI--DALAVAYGVAMN 371

QY 171 GTRPPLIKNLKPPIESLMTRCWSKDPSPSMEEIVK 207  
DB 372 KTLPIPTCTCPBPFARLIECWDPDHGRBDFGSILK 408

RESULT 7  
US-09-221-235-5  
;; Sequence 5, Application US/09221235  
;; Patent No. 6043040  
;; GENERAL INFORMATION:  
;; APPLICANT: Acton, Susan  
;; TITLE OF INVENTION: NOVEL CSAPEK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
;; FILE REFERENCE: NMI-050  
;; CURRENT APPLICATION NUMBER: US/09/221,235  
;; CURRENT FILING DATE: 1998-12-28  
;; EARLIER APPLICATION NUMBER: 09/163,115  
;; EARLIER FILING DATE:  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 455  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-09-221-235-5

Query Match 29.6%; Score 371; DB 3; Length 455;  
Best Local Similarity 37.7%; Pred. No. 2.6e-33;  
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMS 57  
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QY 58 WCLQCSGQVAYLHSMQPKALIHRLDKPNNLLVAGTIVLKI CDPTACDIQTHMTNKGSAW 115  
DB 110 WATVAGKMYLHNEAPVYVYHRLDKSRNVVIAADG-VLKICDPG-ASRFNHTTHMSLV 167

QY 116 GSAAMMAPEVEGNSYSEKCDVPSWGIIMVEVITRRKPFDEIGPAPFRIMAVHNGTRP 174  
DB 168 GTFPMMAPEVYQSLVSEBTDYTSYGAVLWMLTRVEVFGALBG-LQVAVLVEKQERL 225

QY 175 PLIKNLKPPIESLMTRCWSKDPSPSMEEIVKIM 209  
DB 226 TTPSCRSRPAELHQCHEADAKGRBFGKQISIL 260

RESULT 8  
US-09-221-928-5  
;; Sequence 5, Application US/09221928  
;; Patent No. 6121030  
;; GENERAL INFORMATION:  
;; APPLICANT: Acton, Susan  
;; TITLE OF INVENTION: NOVEL CSAPEK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
;; FILE REFERENCE: NMI-050  
;; CURRENT APPLICATION NUMBER: US/09/221,928  
;; CURRENT FILING DATE: 1998-12-28  
;; EARLIER APPLICATION NUMBER: 09/163,115  
;; EARLIER FILING DATE:  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 455  
;; TYPE: PRF  
;; ORGANISM: Homo sapiens  
US-09-221-928-5

Query Match 29.6%; Score 371; DB 3; Length 455;  
Best Local Similarity 37.7%; Pred. No. 2.6e-33;  
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

QY 2 ELRLSRVNHNPVIVLYGACLNPPVCLVMEYAEAGSLYNYLVHGAEPPLPYTAAHAMS 57

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Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPPLLVAAGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVAVIHRDLKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMAPPEVFECSNYSEKCDVFSWGIILMEVITRRKPEDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLITREVPFKGLEG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCMSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPRSFAELHQCWEADAKKRPSPKQIISIL 260

RESULT 9
US-09-221-527-5
; Sequence 5, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; EARLIER FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-221-527-5

Query Match      29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 2.6e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

Qy      2 ELRQLSRVNHNPNIYKLYGACINP--VCLVMEYAEAGSGLYVNLHG--AEPLPYTTAAHAMS 57
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Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPPLLVAAGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVAVIHRDLKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMAPPEVFECSNYSEKCDVFSWGIILMEVITRRKPEDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLITREVPFKGLEG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCMSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPRSFAELHQCWEADAKKRPSPKQIISIL 260

RESULT 10
US-09-221-236-5
; Sequence 5, Application US/09221236
; Patent No. 6146841
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,236
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
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RESULT 11
US-09-221-416-5
; Sequence 5, Application US/09221416
; Patent No. 6153417
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT APPLICATION NUMBER: US/09/221,416
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-221-416-5

Query Match      29.6%; Score 371; DB 3; Length 455;
Best Local Similarity 37.7%; Pred. No. 2.6e-33;
Matches 81; Conservative 40; Mismatches 80; Indels 14; Gaps 8;

Qy      2 ELRQLSRVNHNPNIYKLYGACINP--VCLVMEYAEAGSGLYVNLHG--AEPLPYTTAAHAMS 57
Db      53 EAEILSVLSHRNIIQFYGVILEPPNYGIETVEASIGSLDYINSNRSEEM--DMDHIMT 109
Qy      58 WCLQCSQGVAVYLSHMQPKALIHRLDKPPLLVAAGTVLKICDFGTACDIQTHMTNNK-- 115
Db      110 WATDVAKGMHYLHMEAPVAVIHRDLKSRNVVIAADG-VLKICDFG-ASRFHNHTTHMSLV 167
Qy      116 GSAAMAPPEVFECSNYSEKCDVFSWGIILMEVITRRKPEDEIGPAPRIMW-AVHNGTRP 174
Db      168 GTFPMMAPEVIOQLPVSETCDITYSGVVLMEMLITREVPFKGLEG--LQVAMLVVERKNERL 225
Qy      175 PLIKNLKPRIEISLMTRCMSKDPSPQSPMEIYKIM 209
Db      226 TIPSSCPRSFAELHQCWEADAKKRPSPKQIISIL 260

RESULT 12
US-09-221-245-5
; Sequence 5, Application US/09221245
; Patent No. 6180358
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
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Qy 116 GSAAMWAPVFEFGSNYSKCDVFSWGIIMEVITRRKPPDEIGPAPRIMW-AVANGTRP 174  
Db 168 GFPPMMAPEVIOSLPVSETCDTYSYGVLMEMLTREVPKGLG--LQVAMLVEKNERL 225  
Qy 175 PLIKNLPKPIESIMTRCWSKDPSPRPSMEIVKIM 209  
Db 226 TIPSCPRSFALHQCWEADAKKRPSFKQITISIL 260

Search completed: August 2, 2005, 20:34:06  
Job time : 28.7297 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2005, 20:29:48 ; Search time 83.9955 Seconds  
(without alignments)  
1058.018 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303  
Perfect score: 1252  
Sequence: 1 VELRLQSLRVNHPNIVKLYGA.....MTHLMRYFPADBPLOYPCQ 228

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCTI\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	100.0	336	16	US-10-664-421-135
2	1252	100.0	518	14	US-10-283-023-2
3	1252	100.0	518	15	US-10-386-414-13
4	1252	100.0	579	13	US-10-158-895-4
5	1252	100.0	579	14	US-10-384-743-4
6	1252	100.0	590	13	US-10-158-895-15
7	1252	100.0	590	14	US-10-384-743-15
8	1233.5	98.5	623	17	US-10-732-923-13442
9	1221	97.5	616	17	US-10-732-923-13629
10	1215	97.0	615	17	US-10-732-923-13628
11	815	65.1	268	17	US-10-732-923-13508

12	392.5	31.3	330	16	US-10-664-421-136	Sequence 136, App
13	392.5	31.3	953	15	US-10-369-022-56	Sequence 56, Appl
14	392.5	31.3	954	15	US-10-042-865-98	Sequence 98, Appl
15	392.5	31.3	954	15	US-10-042-865-97	Sequence 97, Appl
16	392.5	31.3	954	15	US-10-263-929-187	Sequence 187, App
17	387.5	31.0	940	18	US-10-840-512-223	Sequence 223, App
18	387.5	31.0	1018	17	US-10-732-923-13436	Sequence 13436, A
19	379	30.3	422	16	US-10-437-963-13604	Sequence 13604, A
20	377	30.1	376	16	US-10-437-963-13612	Sequence 13612, A
21	376	30.0	371	17	US-10-732-923-13608	Sequence 13608, A
22	374.5	29.9	376	15	US-10-424-599-271998	Sequence 271998, A
23	374.5	29.9	2964	17	US-10-732-923-13552	Sequence 13552, A
24	373.5	29.8	603	16	US-10-437-963-135923	Sequence 156923, A
25	373	29.8	357	15	US-10-424-599-252964	Sequence 252964, A
26	373	29.8	415	16	US-10-425-115-351552	Sequence 351552, A
27	373	29.8	426	15	US-10-425-114-60778	Sequence 60778, A
28	373	29.8	433	15	US-10-425-114-57936	Sequence 57936, A
29	372	29.7	289	17	US-10-732-923-13427	Sequence 13427, A
30	372	29.7	415	16	US-10-425-115-351548	Sequence 351548, A
31	372	29.7	426	15	US-10-425-114-55173	Sequence 55173, A
32	372	29.7	454	17	US-10-425-114-58969	Sequence 58969, A
33	372	29.7	802	17	US-10-732-923-13428	Sequence 13428, A
34	372	29.6	312	16	US-10-664-421-137	Sequence 137, App
35	371	29.6	349	14	US-10-106-698-6345	Sequence 6345, App
36	371	29.6	417	15	US-10-425-114-46822	Sequence 46822, A
37	371	29.6	455	9	US-09-757-982-5	Sequence 5, Appl
38	371	29.6	455	15	US-10-094-749-2477	Sequence 2477, Ap
39	371	29.6	455	15	US-10-352-674A-2	Sequence 2, Appl
40	371	29.6	455	17	US-10-786-501-5	Sequence 5, Appl
41	371	29.6	473	15	US-10-296-115-837	Sequence 837, App
42	371	29.6	800	16	US-10-408-765A-1101	Sequence 1101, App
43	371	29.6	800	16	US-10-737-450-66	Sequence 66, Appl
44	371	29.6	800	16	US-10-737-450-66	Sequence 66, Appl
45	371	29.6	800	16	US-10-751-736-64	Sequence 64, Appl

#### ALIGNMENTS

RESULT 1  
US-10-664-421-135 Application US/10664421  
; Sequence 135, Application No. US20040142864A1  
; Publication No. US20040142864A1  
; GENERAL INFORMATION:  
; APPLICANT: BREMER, RYAN  
; APPLICANT: IBRAHIM, PRABHA  
; APPLICANT: KUMAR, ABHINAV  
; APPLICANT: MANDIVAN, VALSAN  
; APPLICANT: MILBURN, MICHAEL V.  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
; FILE REFERENCE: 039363/0703  
; CURRENT APPLICATION NUMBER: US/10/664,421  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/412,341  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/411,398  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 135  
; LENGTH: 336  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-664-421-135

Query Match 100.0%; Score 1252; DB 16; Length 336;  
Best Local Similarity 100.0%; Pred. No. 2e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VELRLQSLRVNHPNIVKLYGACINPVCYMEVAEGSLNVTLHGAPPLRYTAAHMSMCL 60  
DB 76 VELRLQSLRVNHPNIVKLYGACINPVCYMEVAEGSLNVTLHGAPPLRYTAAHMSMCL 135

QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTIVLCIDFGTACDIQTMTNNKGSAAW 120  
DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTIVLCIDFGTACDIQTMTNNKGSAAW 195  
QY 121 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180  
DB 196 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 255  
QY 181 PKPIESLMTRCWSKDPSPRSMEEIVKIMTHLMRYFPGADEPLQYPCQ 228  
DB 256 PKPIESLMTRCWSKDPSPRSMEEIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 2  
US-10-283-023-2  
; Sequence 2: Application US/10283023  
; Publication No. US20030091573A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph M.  
; TITLE OF INVENTION: Methods and compositions for the  
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
; FILE REFERENCE: MP101-239P1RM  
; CURRENT APPLICATION NUMBER: US/10/283,023  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-283-023-2

Query Match 100.0%; Score 1252; DB 14; Length 518;  
Best Local Similarity 100.0%; Pred. No. 3.3e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGTIVLCIDFGTACDIQTMTNNKGSAAW 195  
QY 121 MAPEVEGNSYSEKCDVFSWGIILMEVITRRKPFDEIGGPAFRIMAVHNGTRPPLIKNL 180  
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QY 181 PKPIESLMTRCWSKDPSPRSMEEIVKIMTHLMRYFPGADEPLQYPCQ 228  
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RESULT 3  
US-10-386-414-13  
; Sequence 13: Application US/10386414  
; Publication No. US2004006016A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapeller-Liebermann, Rosana  
; APPLICANT: Robison, Keith E.  
; APPLICANT: White, David  
; APPLICANT: Williamson, Mark W.  
; APPLICANT: Cook, William James  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Macbeth, Kyle J.  
; APPLICANT: Carroll, Joseph M.  
; APPLICANT: Chun, Myoung  
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MP103-0210MTM

; CURRENT APPLICATION NUMBER: US/10/386,414  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: 09/426,282  
; PRIOR FILING DATE: 1999-10-25  
; PRIOR APPLICATION NUMBER: 09/668,266  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/330,970  
; PRIOR FILING DATE: 1999-06-11  
; PRIOR APPLICATION NUMBER: 09/724,599  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 09/860,193  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 10/283,023  
; PRIOR FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 10/010,943  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: 60/254,037  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 09/833,082  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-386-414-13

Query Match 100.0%; Score 1252; DB 15; Length 518;  
Best Local Similarity 100.0%; Pred. No. 3.3e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 256 PKPIESLMTRCWSKDPSPRSMEEIVKIMTHLMRYFPGADEPLQYPCQ 303

RESULT 4  
US-10-158-895-4  
; Sequence 4: Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITAKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158,895  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/J998/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 579



TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-4

Query Match 100.0%; Score 1252; DB 13; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3,7e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFFGADBPLOYPQ 303

RESULT 5  
US-10-384-743-4  
Sequence 4, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIO  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 579  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-4

Query Match 100.0%; Score 1252; DB 14; Length 579;  
Best Local Similarity 100.0%; Pred. No. 3,7e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 76 VELRQLSRVNHNPNIIVKLYGACINPVCLVMEYAEAGSLYNYLHGAEPPLPYTAAHAMSACL 135  
QY 61 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 120  
DB 136 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 195  
QY 121 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 180  
DB 196 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 255  
QY 181 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFFGADBPLOYPQ 228  
DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFFGADBPLOYPQ 303

RESULT 6

US-10-158-895-15  
Sequence 15, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIO  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-15

Query Match 100.0%; Score 1252; DB 13; Length 590;  
Best Local Similarity 100.0%; Pred. No. 3,8e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 76 VELRQLSRVNHNPNIIVKLYGACINPVCLVMEYAEAGSLYNYLHGAEPPLPYTAAHAMSACL 135  
QY 61 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 120  
DB 136 QCSGVAYLHSMOPKALIHDLKPPNLLVAGGTVLKICDGTACDIQTHMTNKGSAAM 195  
QY 121 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 180  
DB 196 MAPEVFGSNYSSEKCDVFSMGIIIMEVITRRKPPDEIGGPAFRIMMAVHNGTRPPLIKNL 255  
QY 181 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFFGADBPLOYPQ 228  
DB 256 PKPIESLMTRCWSKDPSPQSPSMERIIVKIMTHLMRYFFGADBPLOYPQ 303

RESULT 7  
US-10-384-743-15  
Sequence 15, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIO  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 590  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-15

Query Match 100.0%; Score 1252; DB 14; Length 590;

Best Local Similarity 100.0%; Pred. No. 3.8e-110;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 60
DB 76 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 195
QY 121 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 180
DB 196 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 255
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 228
DB 256 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 303

```

## RESULT 8

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US-10-732-923-13442
; Sequence 13442, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13442
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13442

```

Query Match 98.5%; Score 123.5; DB 17; Length 623;  
Best Local Similarity 93.1%; Pred. No. 2.3e-108;  
Matches 228; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

```

QY 1 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 60
DB 76 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 135
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 120
DB 136 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 195
QY 121 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 180
DB 196 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 255
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 223
DB 256 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 315
QY 224 QYPCQ 228
DB 316 QYPCQ 320

```

## RESULT 9

```

US-10-732-923-13629
; Sequence 13629, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

```

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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13629
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-13629

```

Query Match 97.5%; Score 1221; DB 17; Length 616;  
Best Local Similarity 97.4%; Pred. No. 3.5e-107;  
Matches 222; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 60
DB 65 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 124
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 120
DB 125 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 184
QY 121 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 180
DB 185 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 244
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 228
DB 245 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 292

```

## RESULT 10

```

US-10-732-923-13628
; Sequence 13628, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13628
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-13628

```

Query Match 97.0%; Score 1215; DB 17; Length 615;  
Best Local Similarity 96.9%; Pred. No. 1.3e-106;  
Matches 221; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 60
DB 65 VELRQLSRVNHHPNIVLYGACINPVCILWMEYAEAGSLYNVLHGAEPPLPYTTAAHMSWCL 124
QY 61 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 120
DB 125 QCSQGVAYLHSMQPKALIHRLDKPNNLLVAGGTVLKICDFTACDIQTHMTNNKGSAAW 184
QY 121 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 180
DB 185 MAPEVFEAGSNYSKCDVFSWGIILMEVITRRKPFDEIGAPARIMAAVHNGTRPPLIKNL 244
QY 181 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 228
DB 245 PKPISLMTRCWSKDPORPSMEEIVKIMTHLMRYFGADDEPLQYPCQ 292

```

## RESULT 11

```

US-10-732-923-13508

```

```

: Sequence 13508, Application US/10732923
: Publication No. US20050108791A1
: GENERAL INFORMATION:
: APPLICANT: Edgerton, Michael D
: TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
: FILE REFERENCE: 38-15(52796)C
: CURRENT APPLICATION NUMBER: US/10/732,923
: PRIOR FILING DATE: 2003-12-10
: PRIOR APPLICATION NUMBER: 10/310,154
: PRIOR FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 24149
: SEQ ID NO 13508
: LENGTH: 268
: TYPE: PRT
: ORGANISM: Anopheles gambiae str. PEST
US-10-732-923-13508

Query Match      65.1%; Score 815; DB 17; Length 268;
Best Local Similarity 67.4%; Pred. No. 5e-69;
Matches 151; Conservative 23; Mismatches 46; Indels 4; Gaps 3;

Yy 2 ELRLQSLRVNHNIVKLYGACLNP--VCIVMEYAEAGGSILYNYLHGAEPPLPYTAAHMSWC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 36 EVSHLSRAAHNITIELYGACTEKENPFLVMEYADOGSLAKVILH-SRPAPVTTAAHMSKA 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Yy 60 LQCSGVAAYLHSMOPKALIHRLDKRPNNLLVAGGTVLKICDGFACDIIQTHMTNNGSAA 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 95 RQCAEGVAAYLHDMTPRPMIHRLDKRPNNLLVNNGTVLKICDGFVTDSTLMTNNGSAA 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Yy 120 WMAEVEPEGNSYSEKCDVFSWGIIIMEVYTRKPPDEIGGPAFRIMAAVANGTRPPLIKN 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 155 WMAEVEFGSSYTEKCDVFSWGIIIMEVYAREQPFKHL-DTSYALMTMVHOGSRPPLIDH 213
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Yy 180 LPKPIESLMTKCSKDPSPSMETIVKIMTHIMKPFPGADRL 223
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 214 CPKEPLEQLMVRCWMDPISRPSMKEVVNNMALCKLFTGENBPI 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-664-421-136
: Sequence 136, Application US/10664421
: Publication No. US20040142864A1
: GENERAL INFORMATION:
: APPLICANT: BREMER, RYAN
: APPLICANT: IBRAHIM, PRABHA
: APPLICANT: KUMAR, ABHINAV
: APPLICANT: MANDIVAN, VALSAN
: APPLICANT: MILBURN, MICHAEL V.
: TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
: FILE REFERENCE: 039363/0703
: CURRENT APPLICATION NUMBER: US/10/664,421
: CURRENT FILING DATE: 2003-09-16
: PRIOR APPLICATION NUMBER: 60/412,341
: PRIOR FILING DATE: 2002-09-20
: PRIOR APPLICATION NUMBER: 60/411,398
: PRIOR FILING DATE: 2002-09-16
: NUMBER OF SEQ ID NOS: 169
: SOFTWARE: Patentin Ver. 3.2
: SEQ ID NO 136
: LENGTH: 330
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-664-421-136

Query Match      31.3%; Score 392.5; DB 16; Length 330;
Best Local Similarity 40.6%; Pred. No. 8.6e-29;
Matches 88; Conservative 35; Mismatches 77; Indels 17; Gaps 6

Yy 2 ELRLQSLRVNHNIVKLYGACLNP--VCIVMEYAEAGGSILYNYLHGAEPPLPYTAAHMSWC 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 66 EARLFGAIOHPHNPITLARGACLNPPLHCLVMEYARAGSLRVLAGRRVPHV---LVNMA 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

60 LQCSGVAAYLHSMOPKALIHRLDKRPNNLLV-----AGGTVLKICDGFACD-IQTHM 111

```

[illegible]



```

Db      145 EARLFGALQHNPNTIALRGACINPPLCLVMEYARGALSRVLAGRVRPHV---LVNWA 200
QY      60 LQCSQGVAYLHSMQPKALIHRLKPNLLV-----AGTVLXICDFGTACD-IQTHM 111
Db      201 VQVARGMNYLHNDAPVPIIHRDLKSINILLLEAIENHNLAQTVLKITDFGLAREMHKTK 260
QY      112 TNNKGAAMMAPEYPEGSNYSEKCDVPSWGIIMEVITRRKPFDEIGGPAFRIMAY-HN 170
Db      261 MSAAGTYAMMAPEVIRLSLFSKSSDWSFGVLLWELLGDEVYRRI--DALAVAYGVAMN 318
QY      171 GTRPPLIKNLPKPIESLMTRCMSKDPQSQRPSMEIYK 207
Db      319 KLTLPISCTCPFPARLIEECWDPDPHGRPDGSIYK 355

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Search completed: August 2, 2005, 20:42:13  
 Job time : 84.9595 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:33:39 ; Search time 229.541 Seconds

(without alignments)  
1625.295 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303  
Perfect score: 1252  
Sequence: 1 VERKQSLRVNHPNIVKLYGA.....MTHLMRYFGADPELPYPCQ 228

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-O/cgnt2\_1/USPTO.spool/US09830144/funat 02082005 101155 12556/app.query.fasta\_1.654  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdd  
-LIST=45 -DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO MMAP -LARGEOUTERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Issued Patents NA:  
1: /cgnt2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgnt2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgnt2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgnt2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgnt2\_6/ptodata/1/ina/PTUS.COMB.seq:\*  
6: /cgnt2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	1788	3	US-09-529-279-14
2	1252	100.0	1788	4	US-10-158-895-14
3	1252	100.0	2656	2	US-08-685-625A-5
4	1252	100.0	2656	3	US-09-529-279-3
5	1252	100.0	2656	4	US-10-158-895-3
6	1252	100.0	2769	4	US-09-949-016-4031
7	1247	99.6	2443	2	US-08-685-625A-1
8	392.5	31.3	3143	4	US-09-949-016-1327
9	371	29.6	1365	3	US-09-221-235-6
10	371	29.6	1365	3	US-09-221-928-6
11	371	29.6	1365	3	US-09-221-527-6
12	371	29.6	1365	3	US-09-221-236-6

13	371	29.6	1365	3	US-09-221-416-6	Sequence 6, Appli
14	371	29.6	1365	3	US-09-221-245-6	Sequence 6, Appli
15	371	29.6	1365	3	US-09-163-115-6	Sequence 6, Appli
16	371	29.6	1365	3	US-09-221-528-6	Sequence 6, Appli
17	371	29.6	1365	3	US-09-593-553-6	Sequence 6, Appli
18	371	29.6	1365	3	US-09-221-237-6	Sequence 6, Appli
19	371	29.6	1365	4	US-09-757-982-6	Sequence 6, Appli
20	371	29.6	1119	4	US-09-399-588-1	Sequence 1, Appli
21	371	29.6	2120	3	US-09-221-235-4	Sequence 4, Appli
22	371	29.6	2120	3	US-09-221-928-4	Sequence 4, Appli
23	371	29.6	2120	3	US-09-221-527-4	Sequence 4, Appli
24	371	29.6	2120	3	US-09-221-336-4	Sequence 4, Appli
25	371	29.6	2120	3	US-09-221-416-4	Sequence 4, Appli
26	371	29.6	2120	3	US-09-221-245-4	Sequence 4, Appli
27	371	29.6	2120	3	US-09-163-115-4	Sequence 4, Appli
28	371	29.6	2120	3	US-09-221-528-4	Sequence 4, Appli
29	371	29.6	2120	3	US-09-593-553-4	Sequence 4, Appli
30	371	29.6	2120	3	US-09-221-237-4	Sequence 4, Appli
31	371	29.6	2120	4	US-09-757-982-4	Sequence 4, Appli
32	355	28.4	3111	4	US-10-014-882-1	Sequence 1, Appli
33	355	28.4	3111	4	US-10-014-882-1	Sequence 1, Appli
34	355	28.4	3518	4	US-10-014-882-3	Sequence 3, Appli
35	355	28.4	3518	4	US-10-014-882-3	Sequence 3, Appli
36	353.5	28.2	3364	4	US-09-949-016-1927	Sequence 1927, Ap
37	353.5	28.2	3389	1	US-08-395-580-1	Sequence 1, Appli
38	353.5	28.2	3426	1	US-08-205-018-1	Sequence 106, App
39	352.5	28.2	507	4	US-09-270-767-106	Sequence 15389, A
40	352.5	28.2	507	4	US-09-270-767-106	Sequence 15389, A
41	345.5	27.6	3558	4	US-09-949-016-151	Sequence 1518, Ap
42	345.5	27.6	3558	4	US-09-949-016-151	Sequence 1518, Ap
43	338.5	27.0	2505	3	US-09-291-639-3	Sequence 3, Appli
44	338.5	27.0	2505	4	US-09-458-457-3	Sequence 3, Appli
45	338.5	27.0	2505	4	US-09-947-199A-3	Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-529-279-14  
; Sequence 14, Application US/09529279  
; Patent No. 6451617  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIOHKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/09/529, 279  
; CURRENT FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (7)..(1776)  
US-09-529-279-14  
Alignment Scores:  
Pred. No.: 9.04e-146  
Score: 1252.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 3  
Length: 1788  
Matches: 228  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-529-279-14 (1-1788)

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QY      1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20
Db      232 GTAGAGCTTCGGCAGATTATCCCGTGTGAACCAATCTTAATATTGTAAAGCTTTATGAGCC 291
QY      21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db      292 TCGTTGAATCCAGTGTGTCTTGTGATGAAATATGCGAAGGGGGCTCTTTATATATATGTG 351
QY      41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db      352 CTGCATGTGTGTGAACATTGCCATATTATATCTGCTGCCCAAGCAATGAGTTGGTTTGA 411
QY      61 GlnCysSerGlnGlyValAlaIleTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db      412 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGCAATGCAACCCAAAGCCCTAATTACAGG 471
QY      81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuValIleCysAsp 100
Db      472 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGGGCAAGTTCTTAAATAATTTGTAT 531
QY      101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
Db      532 TTGGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTGCTGG 591
QY      121 MetAlaProGluValPheGlyGlySerAsnTyrSerGlyLysCysAspValPheSerTyr 140
Db      592 ATGGCACCCTGAAGTTTGAAGTATGATTAATTCAGTGAATAATGAGTGTTCAGCTGG 651
QY      141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db      652 GGTATTAATCTTGTGGAGATGATTAACGGTGTGGAACCCCTTGTATGATTTGGTGGCCA 711
QY      161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProPheLeuIleLysAsnLeu 180
Db      712 GCTTTCGAAATCAGTGTGGCTGTTCATATATGATCTGACACACCATGATTAATAATTTA 771
QY      181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db      772 CCTAAGCCCATGTGAGACCTGATGATCGTGTGTGCTAAAGATCTTCCAGGCCCT 831
QY      201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db      832 TCATATGAGAAATTTGTGAATAATATGACTCACTTATGCGGTACTTTCCAGAGCAGAT 891
QY      221 GluProLeuGlnTyrProCysGln 228
Db      892 GAGCCATTACAGTATCTTGTGAG 915

RESULT 2
US-10-158-895-14
; Sequence 14, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Alignment Scores:
Pred. No.: 9,04e-146
Score: 1252.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
Matches: 1788
Conservative: 228
Mismatch: 0
Indels: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-14 (1-1788)

QY      1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20
Db      232 GTAGAGCTTCGGCAGATTATCCCGTGTGAACCAATCTTAATATTGTAAAGCTTTATGAGCC 291
QY      21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db      292 TCGTTGAATCCAGTGTGTCTTGTGATGAAATATGCGAAGGGGGCTCTTTATATATATGTG 351
QY      41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db      352 CTGCATGTGTGTGAACATTGCCATATTATATCTGCTGCCCAAGCAATGAGTTGGTTTGA 411
QY      61 GlnCysSerGlnGlyValAlaIleTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80
Db      412 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCACAGCAATGCAACCCAAAGCCCTAATTACAGG 471
QY      81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuValIleCysAsp 100
Db      472 GACCTGAACCAACCAACTTACTGCTGGTGCAGGGGGGCAAGTTCTTAAATAATTTGTAT 531
QY      101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTyr 120
Db      532 TTGGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTGCTGG 591
QY      121 MetAlaProGluValPheGlyGlySerAsnTyrSerGlyLysCysAspValPheSerTyr 140
Db      592 ATGGCACCCTGAAGTTTGAAGTATGATTAATTCAGTGAATAATGAGTGTTCAGCTGG 651
QY      141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
Db      652 GGTATTAATCTTGTGGAGATGATTAACGGTGTGGAACCCCTTGTATGATTTGGTGGCCA 711
QY      161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProPheLeuIleLysAsnLeu 180
Db      712 GCTTTCGAAATCAGTGTGGCTGTTCATATATGATCTGACACACCATGATTAATAATTTA 771
QY      181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db      772 CCTAAGCCCATGTGAGACCTGATGATCGTGTGTGCTAAAGATCTTCCAGGCCCT 831
QY      201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db      832 TCATATGAGAAATTTGTGAATAATATGACTCACTTATGCGGTACTTTCCAGAGCAGAT 891
QY      221 GluProLeuGlnTyrProCysGln 228
Db      892 GAGCCATTACAGTATCTTGTGAG 915

RESULT 3
US-08-685-625A-5
; Sequence 5, Application US/08685625A
; Patent No. 5945301
; GENERAL INFORMATION:
; APPLICANT: UENO, Naoto
; APPLICANT: MATSUMOTO, Kunhiro
; APPLICANT: IRIE, Kenji
; TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL
; TITLE OF INVENTION: TRANSDUCTION SYSTEM

```



NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,625A  
FILING DATE: 24-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-253549  
FILING DATE: 29-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Neut, Donna M.  
REGISTRATION NUMBER: 36,607  
REFERENCE/DOCKET NUMBER: 001560-267  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2656 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 183..1922  
US-08-685-625A-5  
Alignment Scores:  
Pred. No.: 1.68e-145 Length: 2656  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 2  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-08-685-625A-5 (1-2656)  
QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20  
DB 408 GTAGAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATGTAAGCTTATGAGACC 467  
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40  
DB 468 TGCCTGAATCCAGTGTGCTGTGTGAATATGCTGAAGGGGGCTCTTTATATATGTG 527  
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60  
DB 528 CTGATGTGCTGGAACCATCTGCATATTAATCTGCTGCCACGCAATAGATTGGTGTTA 587  
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuIleHisArg 80  
DB 588 CAGTGTCCCAAGAGAGGCTTATCTTCAACAGCAAGCAACCAAGCGTAAATTCACAGG 647  
QY 81 AspleuAspProProAsnLeuLeuValAlaGlyGlyThrValLeuIleCysAsp 100  
DB 648 GACCTGAACCAACCAACTTACTGCTGTGCAAGGGGGGACAGTTCTAAATTTGTGAT 707  
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetTrpAsnAsnIleGlySerAlaAlaTrp 120  
DB 708 TTGGTACAGCTGTGACATTCAGACACACATGACCAATATACAAAGGGGAGTGTCTGTGG 767

QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIleCysAspValPheSerTrp 140  
DB 768 ATGGCACTTCAAGTTTGAAGGTATTAATTAACATGTAAGTGAAGTGTCTTCAAGCTGG 827  
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLeuPheAspGluIleGlyGlyPro 160  
DB 828 GGTATTAATTTCTTGGGAAGATTAACCGCTGGAAACCTTTGATGTGATGGGGCCCA 887  
QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleIleAsnLeu 180  
DB 888 GCTTCCGAATCATGTGGCTGTTCATTAATGATCTGACACACACATGATTAATAATTA 947  
QY 181 ProIleProIleGluSerLeuMetThrArgCysTrpSerIleAspProSerGlnArgPro 200  
DB 948 CTTAAGCCCATTTGAGACCTGATGATCGTTGTGTGCTTAAGAATCCTTCCAGCGCCCT 1007  
QY 201 SerMetGluGluIleValIleGlyIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220  
DB 1008 TCATGTGAGGAATATGTAATTAATGATCACTGATGTGGTACTTCCAGAGCAGAT 1067  
QY 221 GluProLeuGlnTyrProCysGln 228  
DB 1068 GAGCCATTACGATATCCTTGTGAG 1091  
RESULT 4  
US-09-529-279-3  
Sequence 3, Application US/09529279  
Patent No. 645167  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OR INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529, 279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
NUMBER OF SEQ ID NOS: 48.  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2656  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (183)..(1919)  
US-09-529-279-3  
Alignment Scores:  
Pred. No.: 1.68e-145 Length: 2656  
Score: 1252.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 3  
US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-529-279-3 (1-2656)  
QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrGlyAla 20  
DB 408 GTAGAGCTTCGGAGTATCCCGTGTGAACCATCTTAATATGTAAGCTTATGAGACC 467  
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40  
DB 468 TGCCTGAATCCAGTGTGCTGTGTGAATATGCTGAAGGGGGCTCTTTATATATGTG 527  
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60  
DB 528 CTGATGTGCTGGAACCATCTGCATATTAATCTGCTGCCACGCAATAGATTGGTGTTA 587

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QY      61  GlnCysSerGlnGlyValAlaIleuHisSerMetGlnProGlyAlaIleuIleHisArg 80
DB      588  CAGTGTTCACAGAGAGGAGGCTTATCTTCACAGCATCAACCCAAAGCGCTAATTCACAGG 647
QY      81  AspLeuLysProProAsnLeuLeuValAlaGlyIleuValLeuLysIleCysAsp 100
DB      648  GACCTGAACCAACCAACTTACGTGCTGTTGACGGGGGAGACAGTTCTAATAAATTTGTAT 707
QY      101  PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaIleu 120
DB      708  TTGTGTACAGCCTGTGATTCAGACACATGACCAATTAACAAGGAGAGTCTGCTTGG 767
QY      121  MetAlaProGluValPheGluGlySerAsnLysSerGluLysCysAspValPheSerTrp 140
DB      768  ATGGACACCTGAAGTTTAAAGTACTATTAACAGTAAATAATGAGAGTCTTACGCTGG 827
QY      141  GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
DB      828  GGTATTATCTTTGGAAAGTGAACGCGTCGGAACCTTTGATGAGATTGGTGCCCA 887
QY      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
DB      888  GCTTTCAGATCATGTGGGCTGTCAATATGCTACACCACTGATATAAATAATTTA 947
QY      181  ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
DB      948  CCTAAGCCCATGAGAGCGCTGATGACTGTTGTTGCTAAGAATCCTTCCAGAGCCCT 1007
QY      201  SerMetGluGluIleValLysIleMetThrHisLeuMetArgIlePheProGlyAlaAsp 220
DB      1008  TCAATGGAGGAATTTGAAATAATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1067
QY      221  GluProLeuGlnIleYrProCysGln 228
DB      1068  GAGCATTACAGTATCCTTGTCCAG 1091

```

## RESULT 5

US-10-158-895-3

```

; Sequence 3, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHITAKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158, 895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2656
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (183)...(1919)
US-10-158-895-3

```

## Alignment Scores:

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Pred. No.: 1,68e-145
Score: 1252.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

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Length: 2656
Matches: 228
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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```

US-09-830-144-2_copy_76_303 (1-228) x US-10-158-895-3 (1-2656)
QY      1  ValGluLeuArgGlnLeuSerArgValAlaHisProAsnIleValLysLeuTrpGlyAla 20
DB      408  GTAGAGCTTGCGGAGATATCCGTGGAACCATCTTAATATTTGTAAGCTTTATGAGGCC 467
QY      21  CysLeuAsnProValCysLeuValMetGluTrpAlaGluGlyGlySerLeuTrpAsnVal 40
DB      468  TGCTTGAATCATGTGTCTGTGATGAAATATGCTGAAGGGGGCTCTTATATATATG 527
QY      41  LeuHisGlyAlaGluProLeuProTyrTrpThrAlaAlaHisAlaMetSerTrpCysLeu 60
DB      528  CTGATAGTGTCTGAACCATTTGCCATATTAATGCTGCTGCCACGATGATGAGTTT 587
QY      61  GlnCysSerGlnGlyValAlaIleuHisSerMetGlnProGlyAlaIleuIleHisArg 80
DB      588  CAGTGTTCACAGAGAGGAGGCTTATCTTCACAGCATCAACCCAAAGCGCTAATTCACAG 647
QY      81  AspLeuLysProProAsnLeuLeuValAlaGlyIleuValLeuLysIleCysAsp 100
DB      648  GACCTGAACCAACCAACTTACGTGCTGTTGACGGGGGAGACAGTTCTAATAAATTTGTAT 707
QY      101  PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaIleu 120
DB      708  TTGTGTACAGCCTGTGATTCAGACACATGACCAATTAACAAGGAGAGTCTGCTTGG 767
QY      121  MetAlaProGluValPheGluGlySerAsnLysSerGluLysCysAspValPheSerTrp 140
DB      768  ATGGACACCTGAAGTTTAAAGTACTATTAACAGTAAATAATGAGAGTCTTACGCTGG 827
QY      141  GlyIleIleLeuTrpGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160
DB      828  GGTATTATCTTTGGAAAGTGAACGCGTCGGAACCTTTGATGAGATTGGTGCCCA 887
QY      161  AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
DB      888  GCTTTCAGATCATGTGGGCTGTCAATATGCTACACCACTGATATAAATAATTTA 947
QY      181  ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200
DB      948  CCTAAGCCCATGAGAGCGTATGACTGTTGTTGCTAAGAATCCTTCCAGAGCCCT 1007
QY      201  SerMetGluGluIleValLysIleMetThrHisLeuMetArgIlePheProGlyAlaAsp 220
DB      1008  TCAATGGAGGAATTTGAAATAATATGACTCACTTGATGCGGTACTTCCAGAGCAGAT 1067
QY      221  GluProLeuGlnIleYrProCysGln 228
DB      1068  GAGCATTACAGTATCCTTGTCCAG 1091

```

## RESULT 6

US-09-949-016-4031

```

; Sequence 4031, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4031
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Human

```

US-09-949-016-4031

Alignment Scores:  
 Pred. No.: 1,79e-145 Length: 2769  
 Score: 1252.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-949-016-4031 (1-2769)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyGlyVala 20  
 DB 388 GTAGAGCTTCGGCAGTTATCCCGTGAACCATCTTATTTGAAAGCTTATGAGACC 447  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyRAlaGluGlyGlySerLeuTyAsnVal 40  
 DB 448 TGCTGAATCCAGTGTCTTGTGATGAAATATGCTGAAGGGGCTCTTATATATGTG 507  
 QY 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTyPcLeu 60  
 DB 508 CTGCATGTCTGAACCATTCGCATATTAATCTCTGCCCACGCAATGAGTGTGTTTA 567  
 QY 61 GluCysSerGlnGlyValAlaTyLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 DB 568 CAGGTTCCTCCAGAGAGTGTATCTTATCTTCAAGACAGAACCCAAAGCGCTTATTCACAG 627  
 QY 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyTyThrValLeuLysIleCysAsp 100  
 DB 628 GACCTGAACACCAAACTTACTGCTGTTGCAAGGGGGAAGTTCTTAAATTTGATGAT 687  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120  
 DB 688 TTGCTGACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGTGCTTGG 747  
 QY 121 MetAlaProGluValPheGluGlySerAsnTySerGluLysCysAspValPheSerTrp 140  
 DB 748 ATGGCACCCTGAAGTTTGTGAAGTAGTATTAACAGTGAATGATGACGTTCACGCTGG 807  
 QY 141 GlyIleIleLeuTPGluValIleThrArgArgLysProPheAspGluIleGlyGlyPro 160  
 DB 808 GGTATTATCTTGGGAAGTATTAACGCTGCAAAACCTTTGATGATGTGTGGCCCA 867  
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180  
 DB 868 GCTTCCGAATCATGTGGCTGTTCATATGTACTCCACCACTGATATAAAATTTTA 927  
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGluArgPro 200  
 DB 928 CCTAAGCCCATGAGAGCTGATGATCTGTGTGTGTTAAAGATCTTCCACAGGCCCT 987  
 QY 201 SerMetGluGluIleValIleValIleMetThrHisLeuMetArgTyPheProGlyAlaAsp 220  
 DB 988 TCAATGAGGAATTTGAAATTAATGACTCACTTGATGCGGTACTTTCCAGAGACAT 1047  
 QY 221 GluProLeuGlnTyProCysGln 228  
 DB 1048 GAGCATTACAGTATCTGTCTGAG 1071

RESULT 7  
 US-08-685-625A-1  
 Sequence 1, Application US/08685625A  
 Patent No. 5945301  
 GENERAL INFORMATION:  
 APPLICANT: UENO, Naoto  
 APPLICANT: MATSUMOTO, Kunihito  
 APPLICANT: IRIE, Kenji  
 TITLE OF INVENTION: NOVEL KINASE IN TGF-BETA FAMILY SIGNAL  
 NUMBER OF INVENTIONS: 5  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/685,625A  
 FILING DATE: 24-JUL-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-253549  
 FILING DATE: 29-SEP-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meuth, Donna M.  
 REGISTRATION NUMBER: 36,607  
 REFERENCE/DOCKET NUMBER: 001560-267  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2443 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 157..1893  
 US-08-685-625A-1

Alignment Scores:  
 Pred. No.: 6.2e-145 Length: 2443  
 Score: 1247.00 Matches: 227  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.60% Indels: 0  
 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-08-685-625A-1 (1-2443)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyGlyVala 20  
 DB 382 GTGAGGCTCCGGCAGTTGTGCGGTGAACCATCTTAACATTTGATGATGAGACC 441  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyRAlaGluGlyGlySerLeuTyAsnVal 40  
 DB 442 TGCTGAATCCAGTATGTCTTGTGATGAAATATGCAAGGGGCGCTCATTTATATATGTG 501  
 QY 41 LeuHisGlyAlaGluProLeuProTyTyThrAlaAlaHisAlaMetSerTyPcLeu 60  
 DB 502 CTGCATGTCTGAACCATTCCTTACTGACCTGCTCATAGCCATAGCTGTGTTTA 561  
 QY 61 GluCysSerGlnGlyValAlaTyLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 DB 562 CAGTGTTCCTCCAGAGAGTGTCTTACTGCAAGACATGAGCCCAAGCGCTGATTCACAG 621  
 QY 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyTyThrValLeuLysIleCysAsp 100  
 DB 622 GACCTCAAGCTCCCAAACTTCTGCTGTGTTGCAAGAGGAGACAGTTCTTAAATCTGCAT 681  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120  
 DB 682 TTGCTGACAGCTTGTGATATCAACACATGACCAATTAATGAAGAGTGTCTGCTGG 741  
 QY 121 MetAlaProGluValPheGluGlySerAsnTySerGluLysCysAspValPheSerTrp 140  
 DB 742 ATGGCGCTGAAGTGTGTAAGTAGTGAATTAACAGTGAAGAGTGTGATGTCTTCAAGCTGG 801

QY 141 GYIIEIIEIETPRLVALLIETHARGLYSEPRORPHEAPSLIIEGLVGLPYRO 160  
DB 802 GGATATATCTCTGGGAAGATACACCGCGGAACCTTGATGATGATCGTGCCCA 861  
QY 161 AAlphearIIEIETPRAlaValHIsaNGIYThArXProProleuIIElysaNleu 180  
DB 862 GCTTGAATCATATGAGGCTGTTCATTAATGACATCGACACCACTGATCAAAATTTTA 921  
QY 181 ProlYsProIIEgluSerIeueThArXySTIPSerIyAASPProSerGIInArXPro 200  
DB 922 CCTAAGCCCATGAGAGCTGTGATGACACCGCTGTGCTCAAGACCCATCTCAGCGCCCT 981  
QY 201 SerMetGluGluIIEValIySIIIEIETThRIsleuMetArGTYrPheProGIYAlaAsp 220  
DB 982 TCAATGAGAGAAATGTGAAATTAATGACTCACTTGAAGCGGTACTTCCAGAGCGGAT 1041  
QY 221 GluProIeugInTyTProCys 227  
DB 1042 GAGCCATTACAGTATCTTGT 1062

RESULT 8  
US-09-949-016-1327  
/ Sequence 1327, Application US/09949016  
/ Patent No. 6812339  
/ GENERAL INFORMATION:  
/ APPLICANT: VENTER, J. Craig et al.  
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
/ FILE REFERENCE: C1001307  
/ CURRENT APPLICATION NUMBER: US/09/949, 016  
/ PRIOR FILING DATE: 2000-04-14  
/ PRIOR APPLICATION NUMBER: 60/241,755  
/ PRIOR FILING DATE: 2000-10-20  
/ PRIOR APPLICATION NUMBER: 60/237,768  
/ PRIOR FILING DATE: 2000-10-03  
/ PRIOR APPLICATION NUMBER: 60/231,498  
/ NUMBER OF SEQ ID NOS: 207012  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 1327  
/ LENGTH: 3143  
/ TYPE: DNA  
/ ORGANISM: Human  
US-09-949-016-1327

Alignment Scores:  
Pred. No.: 3,498-38 Length: 3143  
Score: 392.50 Matches: 88  
Percent Similarity: 56.68% Conservative: 35  
Best Local Similarity: 40.55% Mismatches: 77  
Query Match: 31.35% Indels: 17  
Gaps: 6

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-949-016-1327 (1-3143)

QY 2 GluIeudArgIInIeuserArGValaenHIsProdenIIEValIyIeueTyTgIYAlaCys 21  
DB 594 GAAGCCCGGCTCTTGAAGCCCTGCAGACCCCAACATATGAGCCCTTGAAGGCGCCCTGC 653  
QY 22 IeuaNPrO-----ValIyIeueValIeMetGluTyTgIYAlaGluGlyGIYSerIeueTyTgN 39  
DB 654 CTCACACCCCAACACCTCTGCTCAAGTGAAGATGATGCCGAGGAGTGCACCTGAGCAGG 713  
QY 40 ValIeueHIsGIYAlaGIuProIeueTyTgTYTThRAlaAlaHIsAlaMeSerTyTgCys 59  
DB 714 GAGCTGGAGGTCGCGGAGTGCACCTCACTG-----CTGGTCAACTGGGCT 761  
QY IeugInCysSerGIInGIYValaIaTyTleuHIsSerMetGInProIyAlaIeueIIEHIs 79  
DB 762 GAGCAGGTCGCGGAGTGAACCTCACTCAACAATGATGCCCTGTCATCATCAAC 821  
QY 80 ArgAerIeueTyTProIaenIeueIeueValI-----AlaGIY 92

DB 822 CGGACCTCAAGTCATCAACATCTGATCTGAGAGCCATCGAGAACCAACACTCGCA 881  
QY 93 GIYThRValIeueTyTleuHIsIeCysAaSPheGIYThRAlaCysAaSP---IIeGIInThRIsmeT 111  
DB 882 GACACGCTGCTCAAGTATCAAGATCAAGACTTGGCTCGCCCGAGTGGCAACAAGCCAG 941  
QY 112 ThRAsaenIyIeGIYSerAlaAlaTyTMeTAlaProGIYValIeHIsGIYIySerIeueTyT 131  
DB 942 ATGAGGCTGCGGAGCTTACAGCTTGATGAGCGCGAGAGTATCGTCTCCCTTC 1001  
QY 132 SerGIuIyIeCysAaSPAlaPheSerTyTgIYIIEIETPRAlaValIIEThRArg 151  
DB 1002 TCCAAAGACATATCTGAGCTTGGAGCTTGGAGCTTGGAGCTGCTGAGCGGAG 1061  
QY 152 IySPProIeAaSPGIuIIEglYIyProIaPheArGIIEMetPRAlaValIIEHisA 170  
DB 1062 GTCCCTTACCGTGAATC-----GACGCTTGGCGCGTATGAGGCTGATGAT 1115  
QY 171 GIYThRArgProProleuIIElysaNleuProIySProlIIEgluSerIeueThRArg 190  
DB 1116 MAGCTACGCTGCCATTCCTTCAAGTGCAGCCCGAGCCCTTGGCCGCTCTGAGAGAA 1175  
QY 191 CySTIPSerIyAaSPProSerGIInArXProSerMetGluGIuIIEValIyS 207  
DB 1176 TCTGGAGCCAGACCCCAAGCGGCGGAGATTTGGTACATCTTGAAG 1226

RESULT 9  
US-09-221-235-6  
/ Sequence 6, Application US/09221235  
/ Patent No. 6043040  
/ GENERAL INFORMATION:  
/ APPLICANT: Action, Susan  
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
/ FILE REFERENCE: MN1-050  
/ CURRENT APPLICATION NUMBER: US/09/221,235  
/ PRIOR FILING DATE: 1998-12-28  
/ EARLIER FILING DATE: 1998-12-28  
/ NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 6  
/ LENGTH: 1365  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)...(1365)  
US-09-221-235-6

Alignment Scores:  
Pred. No.: 4,538-36 Length: 1365  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
Gaps: 8

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-235-6 (1-1365)

QY 2 GluIeudArgIInIeuserArGValaenHIsProdenIIEValIyIeueTyTgIYAlaCys 21  
DB 157 GAGGAGAAATATCTAGTGTCTCACTGATCAAGAAATATCAAGTTATGAGATTAAT 216  
QY 22 IeuaNPrO-----ValIyIeueValIeMetGluTyTgIYAlaGluGlyGIYSerIeueTyTgN 39  
DB 217 CTGAACCTCCCAACATATGATGTCACAGAAATGCTTCTCTGGATCACTCAATGAT 276  
QY 40 ValIeueHIsGIY-----AlaGIuProIeueTyTgTYTThRAlaAlaHIsAlaMeSer 57  
DB 277 TACATTAACAAGTAAAGAAAGATG-----GATATGATCAACATTAATGAC 327  
QY 58 TrpCysIeugInCysSerGIInGIYValaIaTyTleuHIsSerMetGInProIyAlaIeue 77

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Db 328 TGGGCCACTGATGATGACCAAGAAATGATATTATTAATGAGAGCTCCTGTCAAGGTG 387
      :::::|||||
Qy 78 TLehiSaRgApLeuLySProProAsnLeuLeuValAaGlyGlyThrValLeuLyS 97
      :::::|||||
Db 388 ATTCAACAGAACCTCAAGTCAAGAAACGTTGTATATACCTGCTGATGGA---GTACTGAG 444
      :::::|||||
Qy 98 TLeCySaRgPheGlyThrAlaCySaRgPLeGlnThrHisMetThrAsnLeuLyS----- 115
      |||||
Db 445 ATCTGATCCTTGGT---GCCCTCGGTTCCATACCATACACACACATGCTCTTGTT 501
      |||||
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTrpSerGluLyS 135
      |||||
Db 502 GGAACCTTCCCATGATGATGCTCCCAAGATTAATCAAGATGCTCCCTGTGTCAGAACTGT 561
      |||||
Qy 136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgArgLySProPheAsp 155
      |||||
Db 562 GACACATATTCCTTATGCTGCTCTGGAAGATGCTAACAGAGGAGTCCCTTTAAA 621
      |||||
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
      :::::|||||
Db 622 GGTTCGAGAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACGAGAGATTA 675
      |||||
Qy 175 ProLeuIleLySaLeuLeuProLySProIleGluSerLeuMetThrArgCySTrpSerLyS 194
      |||||
Db 676 ACCATTCCAGACAGCTTGCCTCCAGAAAGTTTGTCTGATCACTGTTACATCACTGTGGAACT 735
      |||||
Qy 195 AspProSerGlnArgProSerMetGluGluIleValLySLeuMet 209
      |||||
Db 736 GATCCCAAGAAACGCGCATCATTCACAGCAATCATTCATCACTCG 780
      |||||
RESULT 10
US-09-221-928-6
; Sequence 6, Application US/09221928
; Patent No. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,928
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-928-6

Alignment Scores:
Pred. No.: 4.53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-928-6 (1-1365)
Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLySLeuTrpGlyValaCys 21
      |||||
Db 157 GAGGAGAAATTAATCTAGTCTCTCACTACACAGAAACATATCACTTTTATGAGATTAAT 216
      |||||
Qy 22 LeuAsnPro-----ValCyLeuValMetGluTrpAlaGluGlyGlySerLeuTrpAsn 39
      |||||
Db 217 CTGGAACCTCCCACTATGTCATGTGTACAGAAATATGCTTCTCTGGATCACTTATGAT 276
      |||||
Qy 40 ValLeuHisGly-----AlaGluProLeuProLySProIleValHisAlaHisAlaMetSer 57
```

```
Db 277 TACATTAAACAGTAACAGAGTGAAGATG-----GATATGATCACTTATATACC 327
      :::::|||||
Qy 58 TrpCyLeuGlnCySserGlnGlyValAlaTyLeuHisSerMetGlnProLySAlaLeu 77
      :::::|||||
Db 328 TGGGCCACTGATGATGACCAAGAAATGATATTATTAATGAGAGCTCCTGTCAAGGTG 387
      :::::|||||
Qy 78 TLehiSaRgApLeuLySProProAsnLeuLeuValAaGlyGlyThrValLeuLyS 97
      :::::|||||
Db 388 ATTCAACAGAACCTCAAGTCAAGAAACGTTGTATATACCTGCTGATGGA---GTACTGAG 444
      :::::|||||
Qy 98 TLeCySaRgPheGlyThrAlaCySaRgPLeGlnThrHisMetThrAsnLeuLyS----- 115
      |||||
Db 445 ATCTGATCCTTGGT---GCCCTCGGTTCCATACCATACACACACATGCTCTTGTT 501
      |||||
Qy 116 GlySerAlaAlaTrpMetAlaProGluValPheGluGlySerAsnTrpSerGluLyS 135
      |||||
Db 502 GGAACCTTCCCATGATGATGCTCCCAAGATTAATCAAGATGCTCCCTGTGTCAGAACTGT 561
      |||||
Qy 136 AspValPheSerTrpGlyIleLeuTrpGluValIleThrArgArgLySProPheAsp 155
      |||||
Db 562 GACACATATTCCTTATGCTGCTCTGGAAGATGCTAACAGAGGAGTCCCTTTAAA 621
      |||||
Qy 156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
      :::::|||||
Db 622 GGTTCGAGAGA-----TTACAAGTAGCTTGCTGTAGTGAAGAAAAACGAGAGATTA 675
      |||||
Qy 175 ProLeuIleLySaLeuLeuProLySProIleGluSerLeuMetThrArgCySTrpSerLyS 194
      |||||
Db 676 ACCATTCCAGACAGCTTGCCTCCAGAAAGTTTGTCTGATCACTGTTACATCACTGTGGAACT 735
      |||||
Qy 195 AspProSerGlnArgProSerMetGluGluIleValLySLeuMet 209
      |||||
Db 736 GATCCCAAGAAACGCGCATCATTCACAGCAATCATTCATCACTCG 780
      |||||
RESULT 11
US-09-221-527-6
; Sequence 6, Application US/09221527
; Patent No. 6146832
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: NMI-050
; CURRENT APPLICATION NUMBER: US/09/221,527
; EARLIER FILING DATE: 1998-12-28
; EARLIER APPLICATION NUMBER: 09/163,115
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1365)
US-09-221-527-6

Alignment Scores:
Pred. No.: 4.53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

US-09-830-144-2_COPY_76_303 (1-228) x US-09-221-527-6 (1-1365)
Qy 2 GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValLySLeuTrpGlyValaCys 21
      |||||
Db 157 GAGGAGAAATTAATCTAGTCTCTCACTACACAGAAACATATCACTTTTATGAGATTAAT 216
      |||||
Qy 22 LeuAsnPro-----ValCyLeuValMetGluTrpAlaGluGlyGlySerLeuTrpAsn 39
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Db      217 CTTGAACCTCCCAACTATGTCATGTCACAGAAATAGCTTCTGCGATCACTATGAT 276
Qy      40 ValLeuHieglY-----AlaGluProLeuProTyTYrThrAlaAlaHisAlaMetSer 57
Db      277 TACATTAAACAGTAACAGAGTGAAGATG-----GATATGATATCACTTATGACC 327
Qy      58 TrpCysLeuGlnCysSerGlnGlyValAlaTyLeuHisSerMetGlnProLysAlaLeu 77
Db      328 TGGGCCACTGATGTGCGCAAGAAATGCAATTATTAACATATGAGAGCTCTCTCAAGGTG 387
Qy      78 IleHisArgAspLeuLysProLysLeuLeuValAlaGlyGlyThrValLeuLys 97
Db      388 ATTCACAGAGACCTCAAGTCAGAAACGTTTATAGCTGCTGATGGA---GTACTGAAG 444
Qy      98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db      445 ATCTGTGACTTTGGT---GCCCTCGGTTCCATACCATACACACACATGCTTGTT 501
Qy      116 GlySerAlaAlaTTrpMetAlaProGluValPheGluGlySerAsnTySerGluLysCys 135
Db      502 GGAACCTTCCCATGGATGCTCCACAGAAATTCACAGAGTCTCCCTGTGTGAGAACTTGT 561
Qy      136 AspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db      562 GACACATATTCCTATGCTGATGCTGCTCGAGAGATGCTAACAGAGAGCTCCCTTAAA 621
Qy      156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db      622 GGTTTGAAGA-----TTACAAGTAGCTTGCTTGATGAGAAAAACGAGAGATT 675
Qy      175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db      676 ACCATTCACAGACAGTGGCCCAAGAGTTTGCTGAACTGTTACATCAGTGTGGAGACT 735
Qy      195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db      736 GATGCCAAGAAACGCGCATCTTCACAGCAATATTCATTCCTCG 780

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## RESULT 12

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US-09-221-236-6
/ Sequence 6, Application US/09221236
/ Patent No. 6146841
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: NMI-050
/ CURRENT FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: US/09/221,236
/ EARLIER FILING DATE: 1998-09-29
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1365)
US-09-221-236-6

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## Alignment Scores:

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Pred. No.: 4,53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

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US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-236-6 (1-1365)

Qy 2 GluLeuArgGluLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyValAcys 21

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Db      157 GAGCAGAAATACCTCACTGTCTCCAGTCACAGAAATATCATCTCACTTATGAGTAATT 216
Qy      22 LeuAsnPro-----ValCysLeuValMetGluTyAlaGluGlyLysLeuTyAsn 39
Db      217 CTTGAACCTCCCAACTATGTCATGTCACAGAAATAGCTTCTGCGATCACTATGAT 276
Qy      40 ValLeuHieglY-----AlaGluProLeuProTyTYrThrAlaAlaHisAlaMetSer 57
Db      277 TACATTAAACAGTAACAGAGTGAAGATG-----GATATGATATCACTTATGACC 327
Qy      58 TrpCysLeuGlnCysSerGlnGlyValAlaTyLeuHisSerMetGlnProLysAlaLeu 77
Db      328 TGGGCCACTGATGTGCGCAAGAAATGCAATTATTAACATATGAGAGCTCTCTCAAGGTG 387
Qy      78 IleHisArgAspLeuLysProLysLeuLeuValAlaGlyGlyThrValLeuLys 97
Db      388 ATTCACAGAGACCTCAAGTCAGAAACGTTTATAGCTGCTGATGGA---GTACTGAAG 444
Qy      98 IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
Db      445 ATCTGTGACTTTGGT---GCCCTCGGTTCCATACCATACACACACATGCTTGTT 501
Qy      116 GlySerAlaAlaTTrpMetAlaProGluValPheGluGlySerAsnTySerGluLysCys 135
Db      502 GGAACCTTCCCATGGATGCTCCACAGAAATTCACAGAGTCTCCCTGTGTGAGAACTTGT 561
Qy      136 AspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArgLysProPheAsp 155
Db      562 GACACATATTCCTATGCTGATGCTGCTCGAGAGATGCTAACAGAGAGCTCCCTTAAA 621
Qy      156 GluIleGlyGlyProAlaPheArgIleMetTrp---AlaValHisAsnGlyThrArgPro 174
Db      622 GGTTTGAAGA-----TTACAAGTAGCTTGCTTGATGAGAAAAACGAGAGATT 675
Qy      175 ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTrpSerLys 194
Db      676 ACCATTCACAGACAGTGGCCCAAGAGTTTGCTGAACTGTTACATCAGTGTGGAGACT 735
Qy      195 AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
Db      736 GATGCCAAGAAACGCGCATCTTCACAGCAATATTCATTCCTCG 780

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## RESULT 13

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US-09-221-416-6
/ Sequence 6, Application US/09221416
/ Patent No. 6153417
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan
/ TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
/ FILE REFERENCE: NMI-050
/ CURRENT FILING DATE: 1998-12-28
/ EARLIER APPLICATION NUMBER: US/09/221,416
/ EARLIER FILING DATE: 1998-09-29
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 1365
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1365)
US-09-221-416-6

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## Alignment Scores:

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Pred. No.: 4,53e-36 Length: 1365
Score: 371.00 Matches: 81
Percent Similarity: 56.28% Conservative: 40
Best Local Similarity: 37.67% Mismatches: 80
Query Match: 29.63% Indels: 14
DB: 3 Gaps: 8

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US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-416-6 (1-1365)

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QY      2  GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAlaCys 21
       157  GAGGCAGAAATATCTCAAGTCTCCAGTCAAGAAATCATCCAGTTTATGGAGTATT 216
Db      22  LeuAsnPro-----ValCysLeuValMetGlnTyrIleGluGlyGlySerLeuTyrAsn 39
       217  CTGGAACCTCCCAACTATGGCATTTGTCAGAAATATGCTTCTCGGAGATCATCTTATGAT 276
QY      40  ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
       277  TACATTACAGTACAGAACAGAGAGAGATG-----GATATGATCATATTATAC 327
Db      58  TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeu 77
       328  TGGGCCACTGATGTAGCCAAAGAAATGATATTATTCATATGAGAGCTCTGTCAAGGTG 387
QY      78  IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
       388  ATTACAGAGACCTCAAGTCAAGAAACGTTGTATTAGCTGCTGATGGA---GTACTGAAG 444
QY      98  IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
       445  ATCTGTACCTTTGGT---GCCCTCGGTTCCATTACCATACATACACACATGCTCTGTGTT 501
Db      116  GlySerAlaIatTpmEtAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
       502  GGAATCTTCCCATGATGAGTCCCAAGATTATCCAGAGTCTCCCTGTGTCAAGAACTGT 561
QY      136  AspValPheSerTyrGlyIleIleLeuTyrGluValIleThrArgArgLysProPheAsp 155
       562  GACACATATTCCTATGTGTGTCTCTGAGAGATGCTAACAGAGAGGTCCCTTTTAA 621
Db      156  GluIleGlyGlyProAlaPheArgIleMetTyr---AlaValHisAsnGlyThrArgPro 174
       622  GGTTCGAAGA---TTACAGTAGCTTGGCTTGTAGTGAAGAAAAAACAAGAGATTA 675
QY      175  ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrSerLys 194
       676  ACCATTCCACAGCAGTTCGCCCAAGAGTTTGTCTGACATTCATCACTGTTGGGAAGCT 735
Db      195  AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209
       736  GATGCCAAGAAACGGCCATTCATTCAGCAAAATCATTTCAATCTCG 780

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# RESULT 14

US-09-221-245-6  
 ; Sequence 6, Application US/09221245  
 ; Patent No. 6180358  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan  
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-050  
 ; CURRENT APPLICATION NUMBER: US/09/221,245  
 ; CURRENT FILING DATE: 1998-12-28  
 ; EARLIER APPLICATION NUMBER: US 09/163,115  
 ; EARLIER FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1365  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1365)  
 ; US-09-221-245-6

## Alignment Scores:

Pred. No.: 4,53e-36 Length: 1365  
 Score: 371.00 Matches: 81

Percent Similarity: 56.28% Conservative: 40  
 Best Local Similarity: 37.67% Mismatches: 80  
 Query Match: 29.63% Indels: 14  
 DB: 3 Gaps: 8

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-221-245-6 (1-1365)

```

QY      2  GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIysLeuTyrGlyAlaCys 21
       157  GAGGCAGAAATATCTCAAGTCTCCAGTCAAGAAATCATCCAGTTTATGGAGTATT 216
Db      22  LeuAsnPro-----ValCysLeuValMetGlnTyrIleGluGlyGlySerLeuTyrAsn 39
       217  CTGGAACCTCCCAACTATGGCATTTGTCAGAAATATGCTTCTCGGAGATCATCTTATGAT 276
QY      40  ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
       277  TACATTACAGTACAGAACAGAGAGATG-----GATATGATCATATTATAC 327
Db      58  TrpCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeu 77
       328  TGGGCCACTGATGTAGCCAAAGAAATGATATTATTCATATGAGAGCTCTGTCAAGGTG 387
QY      78  IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
       388  ATTACAGAGACCTCAAGTCAAGAAACGTTGTATTAGCTGCTGATGGA---GTACTGAAG 444
QY      98  IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
       445  ATCTGTACCTTTGGT---GCCCTCGGTTCCATTACCATACATACACACATGCTCTGTGTT 501
Db      116  GlySerAlaIatTpmEtAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
       502  GGAATCTTCCCATGATGAGTCCCAAGATTATCCAGAGTCTCCCTGTGTCAAGAACTGT 561
QY      136  AspValPheSerTyrGlyIleIleLeuTyrGluValIleThrArgArgLysProPheAsp 155
       562  GACACATATTCCTATGTGTGTCTCTGAGAGATGCTAACAGAGAGGTCCCTTTTAA 621
Db      156  GluIleGlyGlyProAlaPheArgIleMetTyr---AlaValHisAsnGlyThrArgPro 174
       622  GGTTCGAAGA---TTACAGTAGCTTGGCTTGTAGTGAAGAAAAAACAAGAGATTA 675
QY      175  ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrSerLys 194
       676  ACCATTCCACAGCAGTTCGCCCAAGAGTTTGTCTGACATTCATCACTGTTGGGAAGCT 735
Db      195  AspProSerGlnArgProSerMetGluGluIleValIysIleMet 209
       736  GATGCCAAGAAACGGCCATTCATTCAGCAAAATCATTTCAATCTCG 780

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# RESULT 15

US-09-163-115-6  
 ; Sequence 6, Application US/09163115A  
 ; Patent No. 6183962  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan  
 ; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MNI-050  
 ; CURRENT APPLICATION NUMBER: US/09/163,115A  
 ; CURRENT FILING DATE: 1998-09-29  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1365  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1365)  
 ; US-09-163-115-6

## Alignment Scores:

Pred. No.: 4,53e-36 Length: 1365  
Score: 371.00 Matches: 81  
Percent Similarity: 56.28% Conservative: 40  
Best Local Similarity: 37.67% Mismatches: 80  
Query Match: 29.63% Indels: 14  
DB: 3 Gaps: 8

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-09-163-115-6 (1-1365)

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QY      2  GluLeuArgGlnLeuSerArgValAlaSerProAsnIleValIysLeuTyrGlyAlaCys 21
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      157  GAGGAGAAATATCTCAGTCTCAGTCAGTCAGAAACATCATCCAGTTTATGAGTAATT 216
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      22  LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn 39
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      217  CTTGAACCTCCCAACTATGACATATGCTCTCTGGAATATGCTCTGGAATATGCTCTATGAT 276
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      40  ValLeuHisGly-----AlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSer 57
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      277  TACATTAAACAGTAACAGAGTAGAGATG-----GATATGATCAGATTATGACC 327
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      58  TyrCysLeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIysAlaLeu 77
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      328  TGGGCCACTGATGATGACCAAGAGATGATATTATTAATATGAGAGCTCCTGTCAGAGTG 387
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      78  IleHisArgAspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLys 97
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      388  ATTACAGAGAGCTTCAGAGTCAAGAAACGTTGTATAGCTGCTGATGGA--GTACTGAAG 444
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      98  IleCysAspPheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLys----- 115
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      445  ATCTGTGACTTTGGT--GCCTCGGTCGATCAATACATACACACAGATGCTTGTT 501
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      116  GlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyrSerGluLysCys 135
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      502  GGAACCTTCCATGATGAGCTCCAGAGTTATCCAGAGTCTCCCTGTGTCAAGAACTTGT 561
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      136  AspValPheSerTyrGlyIleIleLeuTyrGluValIleThrArgArgLysProPheAsp 155
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      562  GACACATATTCCTATGCTGTGTTCTCTGGAGATGCTACAGAGAGAGTCCCTTTAAA 621
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      156  GluIleGlyGlyProAlaPheArgIleMetTyr--AlaValHisAsnGlyThrArgPro 174
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      622  GGTTTGGAGGA-----TTACAAGTAGCTTGCTGTAGTGAGAAAAAAGAGAGATTAA 675
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      175  ProLeuIleLysAsnLeuProLysProIleGluSerLeuMetThrArgCysTyrPheLys 194
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      676  ACCATTCCAGAGCGATTGCCAGAGAGTTTGTGAACCTGTACATCAGTGTGGAGAGCT 735
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      195  AspProSerGlnArgProSerMetGluGluIleValLysIleMet 209
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      736  GATGCCAAGAAACGGCCATCATTCAGCAAAATCATTTCAATCTCTG 780
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

Search completed: August 2, 2005, 20:47:24  
Job time : 236.541 secs



GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:40:24 ; Search time 845,757 Seconds

(without alignments)  
1744.825 Million cell updates/sec

Title: US-09-830-144-2\_COPY\_76\_303

Perfect score: 1252  
Sequence: 1 VELRQLSRVHNPVIVKLYGA.....MTHLMRYFPADSEPLQYPCQ 228

## Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame\_plus.p2n.model -DEV=x1h  
-Q=/cg2\_1/USPRO pool/US09830144/runat 02082005 101156 12592/app query.fasta\_1.654  
-DB=Published Applications NA -QPM=fastlap -SUPFIX=p2n.rmpb -MINMATCH=0.1  
-LOOPC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09830144 @CGN 1 1 1041 @runat 02082005 101156 12592  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database : Published Applications NA:\*

1: /cg2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cg2\_6/ptodata/1/pubpna/US06\_PCT\_NEW\_PUB.seq:\*  
3: /cg2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
4: /cg2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cg2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
6: /cg2\_6/ptodata/1/pubpna/US08\_PCT\_NEW\_PUB.seq:\*  
7: /cg2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
8: /cg2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cg2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cg2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cg2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cg2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
13: /cg2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
15: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
18: /cg2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cg2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
20: /cg2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
21: /cg2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
22: /cg2\_6/ptodata/1/pubpna/US10F\_NEW\_PUB.seq:\*  
23: /cg2\_6/ptodata/1/pubpna/US10F\_NEW\_PUB.seq:\*  
24: /cg2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*  
25: /cg2\_6/ptodata/1/pubpna/US11A\_NEW\_PUB.seq:\*  
26: /cg2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
/cg2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1252	100.0	1705	14 US-10-283-023-1	Sequence 1, Appl1
2	1252	100.0	1705	14 US-10-283-023-3	Sequence 1, Appl1
3	1252	100.0	1705	17 US-10-386-414-12	Sequence 12, Appl1
4	1252	100.0	1788	13 US-10-158-895-14	Sequence 14, Appl1
5	1252	100.0	1788	16 US-10-384-743-14	Sequence 14, Appl1
6	1252	100.0	2656	13 US-10-158-895-3	Sequence 3, Appl1
7	1252	100.0	2656	16 US-10-384-743-3	Sequence 3, Appl1
8	1252	100.0	2769	18 US-10-343-710-107	Sequence 107, App
9	392.5	31.3	2865	18 US-10-263-929-85	Sequence 85, Appl1
10	392.5	31.3	3138	17 US-10-369-022-55	Sequence 55, Appl1
11	392.5	31.3	3435	16 US-10-210-120-86	Sequence 86, Appl1
12	392.5	31.3	3435	22 US-10-909-035-86	Sequence 86, Appl1
13	392.5	31.3	3454	9 US-09-969-347-226	Sequence 226, App
14	392.5	31.3	3454	15 US-10-171-581-312	Sequence 312, App
15	392.5	31.3	3454	21 US-10-843-641A-8355	Sequence 8355, App
16	387.5	31.0	3476	22 US-10-840-512-109	Sequence 109, App
17	379	30.3	1794	19 US-10-437-963-30121	Sequence 30121, App
18	377	30.1	1540	19 US-10-437-963-73129	Sequence 73129, App
19	374.5	29.9	3238	18 US-10-424-599-129156	Sequence 129156, App
20	373.5	29.8	2328	19 US-10-437-963-54440	Sequence 54440, App
21	373	29.8	1926	18 US-10-425-114-22688	Sequence 22688, App
22	373	29.8	2029	18 US-10-425-114-34394	Sequence 34394, App
23	373	29.8	2091	18 US-10-424-599-110122	Sequence 110122, App
24	373	29.8	2793	20 US-10-425-115-166889	Sequence 166889, App
25	372.5	29.8	3619	18 US-10-112-944-15	Sequence 15, Appl1
26	372.5	29.8	3717	17 US-10-210-130-129	Sequence 129, App
27	372	29.7	1814	18 US-10-425-114-3589	Sequence 3589, App
28	372	29.7	1903	18 US-10-425-114-30893	Sequence 30893, App
29	372	29.7	2106	20 US-10-425-115-166885	Sequence 166885, App
30	371.5	29.7	3092	17 US-10-042-865-15	Sequence 15, Appl1
31	371	29.6	1065	15 US-10-106-698-2068	Sequence 2068, App
32	371	29.6	1365	9 US-09-757-982-6	Sequence 6, Appl1
33	371	29.6	1365	21 US-10-786-501-6	Sequence 6, Appl1
34	371	29.6	1718	18 US-10-425-114-11340	Sequence 11340, App
35	371	29.6	2119	18 US-10-352-674A-1	Sequence 1, Appl1
36	371	29.6	2120	9 US-09-757-982-4	Sequence 4, Appl1
37	371	29.6	2120	21 US-10-786-501-4	Sequence 4, Appl1
38	371	29.6	2191	17 US-10-296-115-98	Sequence 98, Appl1
39	371	29.6	2251	17 US-10-094-749-838	Sequence 838, App
40	371	29.6	2455	20 US-10-737-450-65	Sequence 65, Appl1
41	371	29.6	3767	20 US-10-751-736-1	Sequence 1, Appl1
42	370.5	29.6	2207	18 US-10-425-114-22955	Sequence 22955, App
43	370.5	29.6	2866	20 US-10-425-115-36020	Sequence 36020, App
44	370	29.6	1942	18 US-10-425-114-28428	Sequence 28428, App
45	370	29.6	1997	18 US-10-425-114-30767	Sequence 30767, App

## ALIGNMENTS

RESULT 1  
US-10-283-023-1  
; Sequence 1, Application US/10283023  
; Publication No. US2003091573A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroli, Joseph M.  
; TITLE OF INVENTION: Methods and compositions for the  
; TITLE OF INVENTION: diagnosis and treatment of hematological disorders using  
; FILE REFERENCE: MP101-2391RM  
; CURRENT APPLICATION NUMBER: US/10/283,023  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 60/335,044  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 1
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-283-023-1

Alignment Scores:
Pred. No.: 2,94e-152 Length: 1705
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-283-023-1 (1-1705)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleuLeuTyrGlyAla 20
Db 226 GTAGAGCTTCGGCAGATTATCCGCTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 285
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db 286 TECTTGAATCCAGTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAATGTG 345
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 346 CTGCATGTGCTGGAACCATTTGCCATATATCTGCTGCCACGCAATGAGTTGGTGTTA 405
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIlySalAlaLeuIleHisArg 80
Db 406 CAGTGTCCCAAGGAGGTGGCTTATCTTCACAGCATGCAACCAAGGCTTAATTCACAGG 465
QY 81 AspleuIysProProAsnIleuLeuValAlaGlyGlyThrValIleuIysIleCysAsp 100
Db 466 GACCTGAAACCAACCAAACTTACTGCTGTCAGGGGGAGACAGTTCTTAAAAATTTGTGAT 525
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTyr 120
Db 526 TTGTGTACAGCCTGTGACATTCAACACACATGACCAATTAACAAGGGAGTGTGCTTGG 585
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTyr 140
Db 586 ATGGCACCCTGAGTTTGAAGGTAGTAATTAACAGTAATAAATGTGACGCTTCACACTGG 645
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgIysProPheAspGluIleGlyIlePro 160
Db 646 GGTATATATCTTTGGGAAGTGAATACGCGCGAAACCTTTGATGAGATTGTGGCCCA 705
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleIysAsnLeu 180
Db 706 GCTTCCGAAATCAATGAGGCTGTTCATTAATGATGACTGACCAACCATGATTAATAATTTA 765
QY 181 ProIysProIleGluSerLeuMetThrArgCysTyrSerIlyAspProSerGlnArgPro 200
Db 766 CTTAAGCCCATTAAGAGCCTGATGACTCGTTGTGTGTTAAGATCTTTCCAGGCGCTT 825
QY 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 826 TCAATGAGAGAAATTTGTAAAAATATGACTCACTGATGCGGTACTTTCCAGAGACAGAT 885
QY 221 GluProLeuGlnTyrProCysGln 228
Db 886 GAGCCATTACAGTATCTTGTGACG 909

RESULT 2
; Sequence 3, Application US/10283023
; Publication No. US20030091573A1
; GENERAL INFORMATION:
; APPLICANT: Caroll, Joseph M.
; TITLE OF INVENTION: Methods and compositions for the
; diagnosis and treatment of hematological disorders using
; TITLE OF INVENTION: 16319
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; FILE REFERENCE: MP101-239P1RM
; CURRENT APPLICATION NUMBER: US/10/283,023
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1557)
US-10-283-023-3

Alignment Scores:
Pred. No.: 2,94e-152 Length: 1705
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-283-023-3 (1-1705)

QY 1 ValGluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleuLeuTyrGlyAla 20
Db 226 GTAGAGCTTCGGCAGATTATCCGCTGTGAACCATCTTAATTTGTAAGCTTTATGAGCC 285
QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40
Db 286 TECTTGAATCCAGTGTGCTTGTGATGGAATAATGCTGAAGGGGCTCTTTATATAATGTG 345
QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 346 CTGCATGTGCTGGAACCATTTGCCATATATCTGCTGCCACGCAATGAGTTGGTGTTA 405
QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProIlySalAlaLeuIleHisArg 80
Db 406 CAGTGTCCCAAGGAGGTGGCTTATCTTCACAGCATGCAACCAAGGCTTAATTCACAGG 465
QY 81 AspleuIysProProAsnIleuLeuValAlaGlyGlyThrValIleuIysIleCysAsp 100
Db 466 GACCTGAAACCAACCAAACTTACTGCTGTCAGGGGGAGACAGTTCTTAAAAATTTGTGAT 525
QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnIysGlySerAlaAlaTyr 120
Db 526 TTGTGTACAGCCTGTGACATTCAACACACATGACCAATTAACAAGGGAGTGTGCTTGG 585
QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluIysCysAspValPheSerTyr 140
Db 586 ATGGCACCCTGAGTTTGAAGGTAGTAATTAACAGTAATAAATGTGACGCTTCACACTGG 645
QY 141 GlyIleIleLeuTyrGluValIleThrArgArgIysProPheAspGluIleGlyIlePro 160
Db 646 GGTATATATCTTTGGGAAGTGAATACGCGCGAAACCTTTGATGAGATTGTGGCCCA 705
QY 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleIysAsnLeu 180
Db 706 GCTTCCGAAATCAATGAGGCTGTTCATTAATGATGACTGACCAACCATGATTAATAATTTA 765
QY 181 ProIysProIleGluSerLeuMetThrArgCysTyrSerIlyAspProSerGlnArgPro 200
Db 766 CTTAAGCCCATTAAGAGCCTGATGACTCGTTGTGTGTTAAGATCTTTCCAGGCGCTT 825
QY 201 SerMetGluGluIleValIysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 826 TCAATGAGAGAAATTTGTAAAAATATGACTCACTGATGCGGTACTTTCCAGAGACAGAT 885
QY 221 GluProLeuGlnTyrProCysGln 228
Db 886 GAGCCATTACAGTATCTTGTGACG 909
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RESULT 3
US-10-386-414-12
; Sequence 12, Application US/10386414
; Publication No. US2004000616A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; FILE REFERENCE: MP103-0210NMIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-386-414-12

Alignment Scores:
Pred. No.: 2,94e-152 Length: 1705
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-386-414-12 (1-1705)
QY 1 ValGluLeuArgGlnLeuSerArgValAlaSerProAlaLeuValLeuTyrcjVala 20
DB 226 GTAGAGCTTCGCGAGTATACCGGTGAGCAACATCTTAATATTGTAACCTTTATGAGACC 285
QY 21 CysLeuAnProValCysLeuValMetGluTyraLagLugLysSerLeuTyraAnVal 40
DB 286 TGCTTGATTCAGATGTGTCTGTATGATGATGCTGAAGGGGCTCTTTATATATATG 345
QY 41 LeuHISGlyAlaGluProLeuProTyrtThraIaaIaHISAlaMetSerThrcysLeu 60
DB 346 CTGACTGGTGGCAACCATGTCATATTACTGCTGCCCAAGCAATGAGTGGGTTTAA 405
QY 61 GlnCysSerGlnGlyValAlaTyrlLeuHISSerMetGlnProLysAlaLeuIleHISArg 80
DB 406 CAGTGTCCCAAGAGATGGCTTATCTTCACAGCATGCAACCAAGCGCTAATTCACAGG 465
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QY 81 AspleuLySPProAenLeuLeuValAlaGlyGlyThryValLeuLysIleCysASP 100
DB 466 GACCTGAACCAACCAACCTTACTGCTGTCAGGGGGGAGACGTTCTAAAAATTGTGAT 525
QY 101 PheGlyThraIaCysAspIleGlnThrhISMetThraAnLysGlySerAlaIleTP 120
DB 526 TTGGTACAGCTGTGACATTGACACACATGACCAATTAACAGGGAGTGTGCTGG 585
QY 121 MetAlaProGluValPheGlyGlySerAsnTyrsGlnLysCysAspValPheSerTP 140
DB 586 ATGCACACCTTAAGATTTTGAAGTAGTAATTAACGTAAAAAATGACGTGCTGG 645
QY 141 GlyIleIleLeuTPGluValIleThraArgArgLysProPheAspGluIleGlyPro 160
DB 646 GGTATTCTTTCTGGGAAGATGATACCCGTCGAAACCTTTATGATGATTGGGCCCA 705
QY 161 AlaPheArgIleMetTPAlaValIaHISAnGlyThraArgProProLeuIleLysAnLeu 180
DB 706 GCTTCCGAATCATGTGGGCTGTTCAATATGTACTGCACCAACCATGATAAAAATTTA 765
QY 181 ProLysProIleGlySerLeuMetThraGlyTrpSerLysAspProSerGlnArgPro 200
DB 766 CCTAAGCCCATGTGAGACCTGATGACTGTTGTGTCTAAAGATCCTTCCAGCGCCT 825
QY 201 SerMetGluGluIleValLysIleMetThrhISLeuMetArgTyrlPheProGlyAlaASP 220
DB 826 TCAATGAGAGGAATGTGAAATATATACCTTAATGCGGTACTTCCAGAGCAT 885
QY 221 GluProLeuGlnTyrlProCysGln 228
DB 886 GAGCCATTACAGTATCCTTGTGCAG 909

RESULT 4
US-10-158-895-14
; Sequence 14, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAUYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1776)
US-10-158-895-14

Alignment Scores:
Pred. No.: 3.14e-152 Length: 1788
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-158-895-14 (1-1788)
QY 1 ValGluLeuArgGlnLeuSerArgValAlaSerProAlaLeuValLeuTyrcjVala 20
```

```
Db 232 GTAGAGCTTCGGAGTATCCCGTGAACCACTTAATATGTAAGCTTATGAGGCC 291
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TGCTGAATCCAGTGTGCTTGATGATGAAATATGCTGAAGGGGGCTCTTATATATATG 351
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGCATGATGCTGAACCATTCATATTAATGCTGCGCCACGCAATGATGATGTTTA 411
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuHisArg 80
Db 412 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCAACAGATGCAACCCAAAGCGCTAATTCACAG 471
Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 472 GACCTGAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTMAAATTTGTAT 531
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisSerMetGlnProValAlaLeuHisArg 120
Db 532 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGGCTTGG 591
Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 592 ATGGCACTGAAGTTTGAAGTAGTATTACAGTGAAATATGACGCTTCAAGCTCG 651
Qy 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATTTATCTTTGGGAAAGTATTAACGGGTGGAAACCTTTGATGATGGTGGCCCA 711
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 712 GCTTTCGAATCATGTGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 771
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTAGAGCTGATGACTCGTTGGTCTMAAAGATCTTCCAGCGCCCT 831
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 832 TCATGAGAGGAATTTGGAAATATATGACTCACTTGATGCGGTACTTCCAGAGAGAT 891
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCCTGTGCAG 915

RESULT 5
US-10-384-743-14
; Sequence 14, Application US/10384743
; Publication No. US20030162228A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/384,743
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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LOCATION: (7) .. (1776)
US-10-384-743-14

Alignment Scores:
Pred. No.: 3,14e-152 Length: 1788
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-384-743-14 (1-1788)

Qy 1 ValGluLeuArgGluLeuSerArgValAlaHisProAsnIleValLysLeuTyrGlyAla 20
Db 232 GTAGAGCTTCGGAGTATCCCGTGAACCACTTAATATGTAAGCTTATGAGGCC 291
Qy 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlySerLeuTyrAsnVal 40
Db 292 TGCTGAATCCAGTGTGCTTGATGATGAAATATGCTGAAGGGGGCTCTTATATATATG 351
Qy 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCysLeu 60
Db 352 CTGCATGATGCTGAACCATTCATATTAATGCTGCGCCACGCAATGATGATGTTTA 411
Qy 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProValAlaLeuHisArg 80
Db 412 CAGTGTTCCTCCAGAGAGTGGCTTATCTTCAACAGATGCAACCCAAAGCGCTAATTCACAG 471
Qy 81 AspLeuLysProProAsnLeuLeuValAlaGlyGlyThrValLeuLysIleCysAsp 100
Db 472 GACCTGAACCAACCAACTTACTGCTGGTTCAGGGGGGACAGTTCTMAAATTTGTAT 531
Qy 101 PheGlyThrAlaCysAspIleGlnThrHisSerMetGlnProValAlaLeuHisArg 120
Db 532 TTTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAGGGAGTGGCTTGG 591
Qy 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTyr 140
Db 592 ATGGCACTGAAGTTTGAAGTAGTATTACAGTGAAATATGACGCTTCAAGCTCG 651
Qy 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyPro 160
Db 652 GGTATTTATCTTTGGGAAAGTATTAACGGGTGGAAACCTTTGATGATGGTGGCCCA 711
Qy 161 AlaPheArgIleMetTyrAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180
Db 712 GCTTTCGAATCATGTGGGCTGTTCAATATGTAATCTGACACCACTGATTAATAATTA 771
Qy 181 ProLysProIleGluSerLeuMetThrArgCysTyrSerLysAspProSerGlnArgPro 200
Db 772 CCTAAGCCCATGTAGAGCTGATGACTCGTTGGTCTMAAAGATCTTCCAGCGCCCT 831
Qy 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220
Db 832 TCATGAGAGGAATTTGGAAATATATGACTCACTTGATGCGGTACTTCCAGAGAGAT 891
Qy 221 GluProLeuGlnTyrProCysGln 228
Db 892 GAGCCATTACAGTATCCTGTGCAG 915

RESULT 6
US-10-158-895-3
; Sequence 3, Application US/10158895
; Publication No. US20020155624A1
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03
```

PRIOR APPLICATION NUMBER: US/09/529,279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 2656  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (183)..(1919)  
 US-10-158-895-3

Alignment Scores:  
 Pred. No.: 5,44e-152 Length: 2656  
 Score: 1252.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-158-895-3 (1-2656)

QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAla 20  
 DB 408 GTAGAGCTTCGGCAGGTTATCCCGTGTGACCATCTAATATGTAAGCTTATGAGACC 467  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40  
 DB 468 TGCTTGAATCCAGGTGCTCTGTGATGGAATATGCTGAAAGGGGCTCTTTATATATGTG 527  
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60  
 DB 528 CTGATGATGCTGAAACCATTCGCAATATTAATCTGCTGCCAGCAAGAGTGGTGTGTTA 587  
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 DB 588 CAGGTTCCTCCAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCCTAATTCACAGG 647  
 QY 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyTyrValLeuLysIleCysAsp 100  
 DB 648 GACCTGAAACCAACAACTTACTGCTGCTGCAAGGGGAGACAGTTCTAATAAATTTGTGAT 707  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120  
 DB 708 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTGCTGTGG 767  
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140  
 DB 768 ATGGACCTGAAGATTGTAAGAGTAATTAACAGTGAATAATGTAAGCTTTCAGCTGG 827  
 QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyCysPro 160  
 DB 828 GGTATTAATCTTTGGGAAGTAAACGGGTGCAAAACCTTTGATGAGATGGTGCCCA 887  
 QY 161 AlaPheArgIleMetTrpAlaValHisAsnGlyThrArgProProLeuIleLysAsnLeu 180  
 DB 888 GCTTCCCAATCATCTGGCTGTTCATATGATCTGACCAACCACTAATAAATAATTTA 947  
 QY 181 ProLysProIleGluSerLeuMetThrArgCysTrpSerLysAspProSerGlnArgPro 200  
 DB 948 CTTAAGCCCATTTGAAGCTGATGCTGCTTTGTGCTTAAGATCTTCCAGAGGCCCT 1007  
 QY 201 SerMetGluGluIleValLysIleMetThrHisLeuMetArgTyrPheProGlyAlaAsp 220  
 DB 1008 TCAATGAGAGAAATGTGAAATAATATGACTCACTTGAAGCGGTACTTCCAGAGACAGAT 1067  
 QY 221 GluProLeuGlnTyrProCysGln 228  
 |||||

DB 1068 GAGCCATTACAGTATCTTGTGAG 1091

RESULT 7

US-10-384-743-3  
 Sequence 3, Application US/10384743  
 Publication No. US20030162228A1  
 GENERAL INFORMATION:  
 APPLICANT: ONO, KOICHIRO  
 APPLICANT: TSUCHIYA, MASAYUKI  
 APPLICANT: OHTOMO, TOSHIHIKO  
 TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
 FILE REFERENCE: 053466/0278  
 CURRENT APPLICATION NUMBER: US/10/384,743  
 CURRENT FILING DATE: 2003-03-11  
 PRIOR APPLICATION NUMBER: US/09/529,279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 2656  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (183)..(1919)  
 US-10-384-743-3

Alignment Scores:  
 Pred. No.: 5,44e-152 Length: 2656  
 Score: 1252.00 Matches: 228  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 16 Gaps: 0

US-09-830-144-2\_COPY\_76\_303 (1-228) x US-10-384-743-3 (1-2656)

QY 1 ValGluLeuAArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyGlyAla 20  
 DB 408 GTAGAGCTTCGGCAGGTTATCCCGTGTGACCATCTAATATGTAAGCTTATGAGACC 467  
 QY 21 CysLeuAsnProValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsnVal 40  
 DB 468 TGCTTGAATCCAGGTGCTCTGTGATGGAATATGCTGAAAGGGGCTCTTTATATATGTG 527  
 QY 41 LeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTrpCysLeu 60  
 DB 528 CTGATGATGCTGAAACCATTCGCAATATTAATCTGCTGCCAGCAAGAGTGGTGTGTTA 587  
 QY 61 GlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHisArg 80  
 DB 588 CAGGTTCCTCCAGAGAGTGGCTTATCTTACAGCATGCAACCAAGCCTAATTCACAGG 647  
 QY 81 AspleuLysProProAsnLeuLeuValAlaGlyGlyTyrValLeuLysIleCysAsp 100  
 DB 648 GACCTGAAACCAACAACTTACTGCTGCTGCAAGGGGAGACAGTTCTAATAAATTTGTGAT 707  
 QY 101 PheGlyThrAlaCysAspIleGlnThrHisMetThrAsnAsnLysGlySerAlaAlaTrp 120  
 DB 708 TTTGGTACAGCCTGTGACATTCAGACACATGACCAATTAACAGGGAGTGTGCTGTGG 767  
 QY 121 MetAlaProGluValPheGluGlySerAsnTyrSerGluLysCysAspValPheSerTrp 140  
 DB 768 ATGGACCTGAAGATTGTAAGAGTAATTAACAGTGAATAATGTAAGCTTTCAGCTGG 827  
 QY 141 GlyIleIleLeuTyrGluValIleThrArgArgLysProPheAspGluIleGlyCysPro 160  
 DB 828 GGTATTAATCTTTGGGAAGTAAACGGGTGCAAAACCTTTGATGAGATGGTGCCCA 887

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QY 161 AlaphearglllmetTrrAlaValHlsAenglyThraGProProleuilelysaAnleu 180
DB 888 GCTTTCGATCATGATGGGCTGTTTCATATGCTGACGACCACTGATATAAAATTTTA 947
QY 181 ProlySProlleuSerleuMetThraGysTSPserlysaSPProSeGlnaArgPro 200
DB 948 CCAAGCCCATGAGAGGCTGATGACTGCTGTTTGGTCTAAAGATCCTTCCAGGCCCT 1007
QY 201 SerMetGluGluIleValIlysiIleMetThriSleuMetArgTyPheProGlyAlaAsp 220
DB 1008 TCAATGAGAGAAATGTGAAATAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 1067
QY 221 GluProleuGlnTyProCyGln 228
DB 1068 GAGCCATTACAGTATCTTGTGAG 1091

RESULT 8
US-10-343-710-107
; Sequence 107, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: WETZELS, Ingrid
; APPLICANT: WENNDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M., K.-H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343, 710
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 2769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-343-710-107

Alignment Scores:
Pred. No.: 5.76e-152 Length: 2769
Score: 1252.00 Matches: 228
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-830-144-2_COPY_76_303 (1-228) x US-10-343-710-107 (1-2769)
QY 1 ValGlnleuAArgGlnleuSerArgValAsnHisProAsnIleValIlyseuTyrgIyAla 20
DB 388 GTAGAGCTTCGGCAGTTATCCGCTGGAACCATCTTAATTTGTAAGCTTTATGAGGCC 447
QY 21 CysleuAsnProValCySleuValMetGluTyAlaGluGlyGlySerleuTyraAsnAl 40
DB 448 TGGTTAAATCCAGTGTGCTCTTGATGATGAAATGCTGAAGGGGGCTTTATATATATG 507
QY 41 LeuHisGlyAlaGluProleuProTyTyThraAlaAlaHisAlaMetSerTrpCySleu 60
DB 508 CTGCAGATGCTGACCACTTGCATTTATCTGCTGCCAGCAATGATGGTGGTTTA 567
QY 61 GlnCySerGlnGlyAlaAlaTyLeuHisSerMetGlnProIlysaAlaLeuIleHisArg 80
DB 568 CAGTGTTCCTCAAGAGTGGCTTATCTTCAAGCATGCAACCAAGCGCTAATTCACAG 627
QY 81 AspLeuIlysaProProAsnleuIleuValAlaGlyGlyThValleuIlyseIlyCysAsp 100
DB 628 GACCTGAACCAACCAACTTACTGCTGTGCAAGGGGAGAGTCTTAATAATTTGTGAT 687
QY 101 PheGlyThraIlyCysAspIleGlnThriSmetThraAsnIlyGlySerAlaAlaTrp 120
DB 688 TTGGTACAGCTGTGACATTCAGACACATGACCAATTAACAAAGGAGTGTCTGTGG 747
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QY 121 MetAlaProGluValPheGluGlySerAenTySerGluIlyCysAspValPheSerTrp 140
DB 748 ATGCACTCGAAGCTTTTGAAGGTAGTAAATTCACAGAAATGTGACCTCTTCAGCTGG 807
QY 141 GlyIleIleuThraGluValIleThraArgGlyPheProPheAspGluIleGlyGlyPro 160
DB 808 GGTATTATTCTTTGGGAAGTGAATACGCTCGGAAACCTTTGATGATGATTTGGTGGCCA 867
QY 161 AlaphearglllmetTrrAlaValHlsAenglyThraGProProleuilelysaAnleu 180
DB 868 GCTTTCGATCATGATGGGCTGTTTCATATGCTGACGACCACTGATATAAAATTTTA 927
QY 181 ProlySProlleuSerleuMetThraGysTSPserlysaSPProSeGlnaArgPro 200
DB 928 CCAAGCCCATGAGAGGCTGATGACTGCTGTTTGGTCTAAAGATCCTTCCAGGCCCT 987
QY 201 SerMetGluGluIleValIlysiIleMetThriSleuMetArgTyPheProGlyAlaAsp 220
DB 988 TCAATGAGAGAAATGTGAAATAATGACTCACTTGATGCGGTACTTTCCAGAGCAGAT 1047
QY 221 GluProleuGlnTyProCyGln 228
DB 1048 GAGCCATTACAGTATCTTGTGAG 1071

RESULT 9
US-10-263-929-85
; Sequence 85, Application US/10263929
; Publication No. US20040067535A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Alzheimer's Disease Linked Genes
; FILE REFERENCE: LSD-07417
; CURRENT APPLICATION NUMBER: US/10/263, 929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-263-929-85

Alignment Scores:
Pred. No.: 6.77e-40 Length: 2865
Score: 392.50 Matches: 88
Percent Similarity: 56.68% Conservative: 35
Best Local Similarity: 40.55% Mismatches: 77
Query Match: 31.35% Indels: 17
DB: 18 Gaps: 6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-263-929-85 (1-2865)
QY 2 GluIleuAArgGlnleuSerArgValAsnHisProAsnIleValIlyseuTyrgIyAlaCys 21
DB 433 GAAAGCCGGCTCTTGGAGCCCTGCAAGACCCCAACATAATTCCTTTAGGGGCGCTGC 492
QY 22 LeuAsnPro-----ValCySleuValMetGluTyAlaGluGlyGlySerleuTyraAsn 39
DB 493 CTCAAGCCCAACCACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 552
QY 40 ValLeuHisGlyAlaGluProleuProTyTyThraAlaAlaHisAlaMetSerTrpCys 59
DB 553 GTGCTGGCAGTGTGCGCGGTCACCTCAAGT-----CTGCTCAACTGGGCT 600
QY 60 LeuGlnCySerGlnGlyAlaAlaTyLeuHisSerMetGlnProIlysaAlaLeuIleHis 79
DB 601 GTGAGAGTGGCCCGGGCAAGAACTACCTACACAAATGATGCCCTGTGCCATCATCCAC 660
QY 80 ArgAspLeuIlysaProProAsnleuIleuVal-----AlaGly 92
DB 661 CCGGACCTCAAGTCCATCAACATCTGATCTGGAAGCCATGAGAACCAACCAACTCGCA 720
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Qy 93 G1yhrVAlleuVv1le1CyAspPheg1Yhr1a1CyAsp---1leG1Th1s1met 111
Db 721 GACACGGGCTGCATMAATACGAGACTTGGCTCCGCCCGGAGTGGACACAAAGCACCCAG 780
Qy 112 ThraenAen1ySG1ySer1a1Ala1rPMe1a1ProG1u1a1PheG1uG1ySer1a1n1Yr 131
Db 781 ATGAGCGGTGGGGGAGCCTAGCGCTGAGTGGGCGGAGGTATCCGTCTCTCTCTCT 840
Qy 132 SerG1u1yCySAspVAlPheSer1rP1y1le1le1e1rP1G1u1a1le1h1r1a1r1a1y 151
Db 841 TCCAAACACAGTGAATCTGAGCTTGGGGGCTGCTGGAGACTGCTGACCGGGAGAG 900
Qy 152 LysP1rPheAspG1u1leG1yG1yP1rOAl1a1PheA1g1leMe1r1P1a1a1l---H1s1a1n 170
Db 901 GTCCCTTACCGGAGATC-----GACGCTTGGCGCGTGGCCGTATAGCGCTGCTATGAT 954
Qy 171 G1yTh1a1r1a1P1rO1e1u1le1yS1a1n1e1u1P1rO1yS1P1rO1le1G1u1Ser1e1u1e1Th1a1r1a1y 190
Db 955 AAGCTGAGCGTCCCATTCCTCCACGTGCGCCGAGCCCTTGGCCCGCTCTGAGAGA 1014
Qy 191 Cy1r1P1rS1e1r1yS1a1P1rO1S1e1r1a1r1P1rO1S1e1r1e1u1le1a1l1yS 207
Db 1015 TGCTGGAGCCAGACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1065

RESULT 10
US-10-369-022-55
; Sequence 55, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33269, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16568, 55054, 16314, 1613, 1675, 9569 OR
; FILE REFERENCE: MP102-027P1R1NOM1TH
; CURRENT APPLICATION NUMBER: US/10/369, 022
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360, 495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370, 121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373, 010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373, 908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377, 717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379, 949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382, 409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385, 280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386, 879
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/387, 536
; PRIOR FILING DATE: 2002-06-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (161)...(3022)
; US-10-369-022-55

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Alignment Scores:	7.68e-40	Length:	3138
Pred. No.:	392.50	Matches:	88
Score:	56.68%	Conservative:	35
Percent Similarity:	40.55%	Mismatches:	77
Best Local Similarity:	31.35%	Indels:	17
Query Match:		Gaps:	6
DB:	17		
US-09-830-144-2_COPY_76_303 (1-228) x US-10-369-022-55 (1-3138)			
QY	2	GLULEuArgrInLeuSerHArgValAlaAsnHisProAsnIleValIysLeuTyRGIValAlaCys	21
DB	593	GAACCCCGCGCTCTTTGGAGCCCTGCACACACCCCAACAAATATGCTTAAAGGCGCTGC	652
QY	22	LeuAsnPro-----ValCysLeuValMetGluTyrAlaGluGlyGlySerLeuTyrAsn	39
DB	653	CTCAACCCCAACACACTCTGCTGTATGATGAGATATCCCGGGGTGTGACATGACGAGG	712
QY	40	ValLeuHisGlyAlaGluProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys	59
DB	713	GTGCTGGAGAGTGGCCGGGTGCACACTCCACATGCTG-----CTGGTCAACTGGAGCT	760
QY	60	LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis	79
DB	761	GTGCAGGAGGCGCGGGGATGAACTACTTACATGATGATCCCTGTGCCATATCTCAC	820
QY	80	ArgAspLeuLysProProAsnIleLeuLeuVal-----AlaGly	92
DB	821	CGGAGCTCAAGTCCATCATCAATCTGTATCTCTGAGGAGCATCGAAGCAACCAACTGCA	880
QY	93	GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet	111
DB	881	GACACGGGTCTCAAGATACACGGACTTGGGCTCCGCGCGAGTGACACAGACCAACCAAG	940
QY	112	ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGluValPheGluGlySerAsnTyr	131
DB	941	ATGACCGCTGGCGGAGCACTTACGCTCGATGAGCGCGGAGTTATCCGTCTCTCCTTTC	1000
QY	132	SerGluLysCysAspValPheSerTyrPylIleIleLeuTyrGluValIleThrArgArg	151
DB	1001	TCCAAACAGCATGATGTCTGAGAGCTCGGGGTCTGCTGTGGAGAGCTCTACCGGGAGG	106
QY	152	LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTyrAlaVal---HisAsn	170
DB	1061	GTCCCTACCGCGAATC-----GACGCTTGGCGCGGTGAGGTGCGGTATGAT	1114
QY	171	GlyThrArgProProLeuIleIleLysAsnLeuProLysProIleGluSerLeuMetThrArg	190
DB	1115	AAGCTGACGTGCGCCATTCCTCCACGTCGCCCGAGCCCTTGGCCGCTCTGGAGGAA	1174
QY	191	CysTyrSerLysAspProSerGlnArgProSerMetGluIleValIys	207
DB	1175	TGCTGGAGACCCAGACCCCAAGTTCGGTAGACATCTTAAG	1225
RESULT 11			
US-10-210-120-86			
Sequence 86, Application US/10210120			
Publication No. US20030175736A1			
GENERAL INFORMATION:			
APPLICANT: Chimaiayan, Arul M.			
APPLICANT: Rubini, Mark A.			
APPLICANT: Sreekumar, Arun			
TITLE OF INVENTION: Expression Profile of Prostate Cancer			
FILE REFERENCE: UM-07221			
CURRENT APPLICATION NUMBER: US/10/210,120			
CURRENT FILING DATE: 2002-08-01			
PRIOR APPLICATION NUMBER: US 60/309,581			
PRIOR FILING DATE: 2001-08-02			
PRIOR APPLICATION NUMBER: US 60/334,468			
PRIOR FILING DATE: 2001-11-15			
NUMBER OF SEQ ID NOS: 123			
SOFTWARE: PatentIn version 3.2			

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; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-86

Alignment Scores:
Pred. No.:      8 71e-40      Length:      3435
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:     31.35%      Indels:     17
DB:              16          Gaps:          6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-210-120-86 (1-3435)

QY      2  GtLeuAArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
DB      721 GAAGCCCGGCTCTTTGGAGCCCTCGACGACCCCAATATATGCCCCCTTAAAGGGGCGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsn 39
DB      781 CTCAACCCCCCAACACCTCTGCTAGTATGAGTATGCCCGGGGGTGGTGCATGACGAG 840
QY      40  ValLeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys 59
DB      841 GTGCTGGAGAGTCCCGGGGTGCCACCTCACTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
DB      889 GTGCAGGTGGCCCGGGGCGATGACTACCTACACATATATGCCCCCTGTGCCCATATCCAC 948
QY      80  ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
DB      949 CGGAGCTTCAGTCCATCAATCACTCTGATCTCGAGGCCATCGAAGAACACCAACTCGCA 1008
QY      93  GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
DB      1009 GACACGGGTCTCAAGATACAGGACTTTCGGCTCGCCCGGAGTGGCAACAGACCAACG 1068
QY      112  ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlnValPheGlnGlySerAsnTyr 131
DB      1069 ATGAGCCCTGCGGGGAGCTACGCTGATGGCGCGAGGTATCCCTCTCCCTCTTC 1128
QY      132  SerGlnLysCysAspValPheSerTyrGlyIleLeuTyrGlnValIleThrArgArg 151
DB      1129 TCCAAAGACAGTATGTTCTGAGCTTGGGGTGTCTGTGGAGAGCTGACGAGGGGAG 1188
QY      152  LysProPheAspGlnIleGlyGlyProAlaPheArgIleMetTyrAlaVal---HisAsn 170
DB      1189 GTCCCTTACCGTAGATC-----GAGCCTTGGCCGTGGCGGTATGGCGGTATGAAT 1242
QY      171  GlyThrArgProProLeuIleLysAsnLeuProLysProIleGlnSerLeuMetThrArg 190
DB      1243 AAGCTGACGCTGCCATTCCTCCACGTCGCCGAGCCCTTTCGCCGCTCTCGAGGAA 1302
QY      191  CysTyrSerLysAspProSerGlnArgProSerMetGlnGlnIleValLys 207
DB      1303 TGCTGGAGCCAGACCCCAACGCGGCGCGAGATTTCGTAGCATTTGAAG 1353

RESULT 12
US-10-909-035-86
; Sequence 86, Application US/10909035
; Publication No. US20050136493A1
; GENERAL INFORMATION:
; APPLICANT: Rubin, Mark A.
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Laxman, Bharathi
; APPLICANT: Sreekanth, Arun
; TITLE OF INVENTION: AMACR Cancer Markers
; FILE REFERENCE: UM-09098
; CURRENT APPLICATION NUMBER: US/10/909,035
; CURRENT FILING DATE: 2004-07-30
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; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-909-035-86

Alignment Scores:
Pred. No.:      8 71e-40      Length:      3435
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:     31.35%      Indels:     17
DB:              22          Gaps:          6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-909-035-86 (1-3435)

QY      2  GtLeuAArgGlnLeuSerArgValAsnHisProAsnIleValLysLeuTyrGlyAlaCys 21
DB      721 GAAGCCCGGCTCTTTGGAGCCCTCGACGACCCCAATATATGCCCCCTTAAAGGGGCGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGlnTyrAlaGlnGlyGlySerLeuTyrAsn 39
DB      781 CTCAACCCCCCAACACCTCTGCTAGTATGAGTATGCCCGGGGGTGGTGCATGACGAG 840
QY      40  ValLeuHisGlyAlaGlnProLeuProTyrTyrThrAlaAlaHisAlaMetSerTyrCys 59
DB      841 GTGCTGGAGAGTCCCGGGGTGCCACCTCACTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrLeuHisSerMetGlnProLysAlaLeuIleHis 79
DB      889 GTGCAGGTGGCCCGGGGCGATGACTACCTACACATATATGCCCCCTGTGCCCATATCCAC 948
QY      80  ArgAspLeuLysProProAsnLeuLeuVal-----AlaGly 92
DB      949 CGGAGCTTCAGTCCATCAATCACTCTGATCTCGAGGCCATCGAAGAACACCAACTCGCA 1008
QY      93  GlyThrValLeuLysIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
DB      1009 GACACGGGTCTCAAGATACAGGACTTTCGGCTCGCCCGGAGTGGCAACAGACCAACG 1068
QY      112  ThrAsnAsnLysGlySerAlaAlaTyrMetAlaProGlnValPheGlnGlySerAsnTyr 131
DB      1069 ATGAGCCCTGCGGGGAGCTACGCTGATGGCGCGAGGTATCCCTCTCCCTCTTC 1128
QY      132  SerGlnLysCysAspValPheSerTyrGlyIleLeuTyrGlnValIleThrArgArg 151
DB      1129 TCCAAAGACAGTATGTTCTGAGCTTGGGGTGTCTGTGGAGAGCTGACGAGGGGAG 1188
QY      152  LysProPheAspGlnIleGlyGlyProAlaPheArgIleMetTyrAlaVal---HisAsn 170
DB      1189 GTCCCTTACCGTAGATC-----GAGCCTTGGCCGTGGCGGTATGGCGGTATGAAT 1242
QY      171  GlyThrArgProProLeuIleLysAsnLeuProLysProIleGlnSerLeuMetThrArg 190
DB      1243 AAGCTGACGCTGCCATTCCTCCACGTCGCCGAGCCCTTTCGCCGCTCTCGAGGAA 1302
QY      191  CysTyrSerLysAspProSerGlnArgProSerMetGlnGlnIleValLys 207
DB      1303 TGCTGGAGCCAGACCCCAACGCGGCGCGAGATTTCGTAGCATTTGAAG 1353

RESULT 13
US-09-969-347-226
; Sequence 226, Application US/09969347
; Patent No. US20020115085A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Cancer Gene Determination and Therapeutic Screening Using Signati
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-69
; CURRENT APPLICATION NUMBER: US/09/969,347
; CURRENT FILING DATE: 2001-10-02
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; PRIOR APPLICATION NUMBER: US/60/237,598
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,604
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 318
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-969-347-226

Alignment Scores:
Pred. No.:      8,78e-40      Length:      3454
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:    31.35%      Indels:      17
DB:              9      Gaps:          6

US-09-830-144-2_COPY_76_303 (1-228) x US-09-969-347-226 (1-3454)

QY      2  GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrglyValaCys 21
       721  GAAGCCCGGCTCTTGGAGCCCTGCAGACCCCAACATTAATGGCCCTTAGGGGGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGluTyrglyValaGluIleGlySerLeuTyraSn 39
       781  CTCAACCCCCACACACTCTGCTGCTAGTAGATGATGCCGGGGTGGTGCACCTAGACAG 840
QY      40  ValLeuHisGlyAlaGluProLeuProTyrrTyrrThraIalaIaHisAlaMetSerTrpCys 59
       841  GTGCTGGCAGGTCCCGGGGTCCACCTCACTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrrLeuHisSerMetGlnProIleValaLeuIleHis 79
       889  GTGCAGGTGGCCCGGGGCATCACTCACTCAACATATGATGCCCTGTGCCCATCATCCAC 948
QY      80  ArgAspLeuIleProProAsnLeuLeuVal-----AlaGly 92
       949  CGGACCTCAAGTCATCATCATCATCTGATCTCGAGGCGCATCGAACAACCACTCGCA 1008
QY      93  GlyThrValLeuIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
       1009  GACACGGGTCTCAAGATCAGCAGACTTCGGCTCGCGCCGAGTGGCACAACAACCAAG 1068
QY      112  ThrAsnAsnIleGlySerAlaIleAlaTrpMetAlaProGluValPheGluGlySerAsnTyrr 131
       1069  ATGAGCGGTGGGGAGCTTACGCTGATGGCGCGGAGTTATCCGTCTCTCTCTTC 1128
QY      132  SerGluIleCysAspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArg 151
       1129  TCCAAAGACATGATGCTGTGAGCTTCGGGGTGGCTGTGGAGCTCTGACGGGGAG 1188
QY      152  LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
       1189  GTCCCTACCGTGAATC-----GACGCTTGGCGGTGGGTGGGTGGGTGGGTGAAT 1242
QY      171  GlyThrArgProProLeuIleIleYasnLeuProIleGlySerLeuMetThrArg 190
       1243  AAGCTGACGCTGCCATTCCTCCACGTCGCGCGGAGCTTTGGCCCGCTCTGTGAGGAA 1302
QY      191  CysTrpSerIleAspProSerGlnArgProSerMetGluIleValIleValIle 207
       1303  TGCTGGAGACCAAGACCCCAAGGGGGGAGATTTCCGTAGCATCTTGAAG 1353
DB

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; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 312
; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X90846
; DATABASE ENTRY DATE: 2001-06-18
; US-10-171-581-312

Alignment Scores:
Pred. No.:      8,78e-40      Length:      3454
Score:          392.50      Matches:      88
Percent Similarity: 56.68%      Conservative: 35
Best Local Similarity: 40.55%      Mismatches: 77
Query Match:    31.35%      Indels:      17
DB:              15      Gaps:          6

US-09-830-144-2_COPY_76_303 (1-228) x US-10-171-581-312 (1-3454)

QY      2  GluLeuArgGlnLeuSerArgValAsnHisProAsnIleValIleLeuTyrglyValaCys 21
       721  GAAGCCCGGCTCTTGGAGCCCTGCAGACCCCAACATTAATGGCCCTTAGGGGGCTGC 780
QY      22  LeuAsnPro-----ValCysLeuValMetGluTyrglyValaGluIleGlySerLeuTyraSn 39
       781  CTCAACCCCCACACACTCTGCTGCTAGTAGATGATGCCGGGGTGGTGCACCTAGACAG 840
QY      40  ValLeuHisGlyAlaGluProLeuProTyrrTyrrThraIalaIaHisAlaMetSerTrpCys 59
       841  GTGCTGGCAGGTCCCGGGGTCCACCTCACTG-----CTGCTCACTGGGCT 888
QY      60  LeuGlnCysSerGlnGlyValAlaTyrrLeuHisSerMetGlnProIleValaLeuIleHis 79
       889  GTGCAGGTGGCCCGGGGCATCACTCACTCAACATATGATGCCCTGTGCCCATCATCCAC 948
QY      80  ArgAspLeuIleProProAsnLeuLeuVal-----AlaGly 92
       949  CGGACCTCAAGTCATCATCATCATCTGATCTCGAGGCGCATCGAACAACCACTCGCA 1008
QY      93  GlyThrValLeuIleCysAspPheGlyThrAlaCysAsp---IleGlnThrHisMet 111
       1009  GACACGGGTCTCAAGATCAGCAGACTTCGGCTCGCGCCGAGTGGCACAACAACCAAG 1068
QY      112  ThrAsnAsnIleGlySerAlaIleAlaTrpMetAlaProGluValPheGluGlySerAsnTyrr 131
       1069  ATGAGCGGTGGGGAGCTTACGCTGATGGCGCGGAGTTATCCGTCTCTCTCTTC 1128
QY      132  SerGluIleCysAspValPheSerTrpGlyIleIleLeuTrpGluValIleThrArgArg 151
       1129  TCCAAAGACATGATGCTGTGAGCTTCGGGGTGGCTGTGGAGCTCTGACGGGGAG 1188
QY      152  LysProPheAspGluIleGlyGlyProAlaPheArgIleMetTrpAlaVal---HisAsn 170
       1189  GTCCCTACCGTGAATC-----GACGCTTGGCGGTGGGTGGGTGGGTGGGTGAAT 1242
QY      171  GlyThrArgProProLeuIleIleYasnLeuProIleGlySerLeuMetThrArg 190
       1243  AAGCTGACGCTGCCATTCCTCCACGTCGCGCGGAGCTTTGGCCCGCTCTGTGAGGAA 1302
QY      191  CysTrpSerIleAspProSerGlnArgProSerMetGluIleValIleValIle 207
       1303  TGCTGGAGACCAAGACCCCAAGGGGGGAGATTTCCGTAGCATCTTGAAG 1353
DB

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RESULT 14
US-10-171-581-312
; Sequence 312, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter

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RESULT 15
US-10-843-641A-8355

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using BW model

Run on: August 2, 2005, 17:23:41 ; Search time 55.8243 Seconds  
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5979.480 Million cell updates/sec

Title: US-09-830-144-3\_COPY\_1338\_1541

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Scoring table:  
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	204	100.0	1560 2 US-08-752-891-5	Sequence 5, Appli
3	204	100.0	1560 2 US-09-144-178-1	Sequence 1, Appli
4	204	100.0	1560 2 US-09-144-178-5	Sequence 5, Appli
5	204	100.0	1560 3 US-09-406-854-1	Sequence 1, Appli
6	204	100.0	1560 3 US-09-406-854-5	Sequence 5, Appli
7	204	100.0	1560 3 US-09-529-279-1	Sequence 1, Appli
8	204	100.0	1560 3 US-10-158-895-1	Sequence 1, Appli
9	204	100.0	1568 3 US-09-529-279-42	Sequence 42, Appli
10	204	100.0	1568 3 US-10-158-895-42	Sequence 42, Appli
11	204	100.0	1569 3 US-09-529-279-10	Sequence 10, Appli
12	204	100.0	1569 3 US-10-158-895-10	Sequence 10, Appli
13	37.2	18.2	1278 4 US-09-252-991A-4932	Sequence 4932, Ap
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15	37.2	18.2	1505 3 US-09-142-481-1	Sequence 1, Appli
16	37.2	18.2	1878 4 US-09-252-991A-4933	Sequence 4933, Ap
17	37.2	18.2	2211 4 US-09-252-991A-4927	Sequence 4927, Ap
18	36.4	17.8	591 4 US-10-101-464A-289	Sequence 289, App
19	36.4	17.8	2380 4 US-10-101-464A-864	Sequence 864, App
20	35.4	17.4	762 4 US-09-252-991A-3481	Sequence 3481, Ap
21	35.4	17.4	1203 4 US-09-252-991A-3468	Sequence 3468, Ap
22	35.4	17.4	1269 4 US-09-252-991A-3470	Sequence 3470, Ap
23	35.4	17.4	45314 4 US-09-949-016-13594	Sequence 13594, A
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25	34	16.7	588 4 US-08-426-630-33	Sequence 33, Appli
26	34	16.7	1896 4 US-08-426-630-33	Sequence 33, Appli
27	34	16.7	4748 4 US-08-426-630-29	Sequence 29, Appli

C 28	33.8	16.6	47981	4	US-09-679-279-1	Sequence 1, Appli
C 29	33.6	16.5	81001	3	US-09-750-580-1	Sequence 1, Appli
C 30	32.8	16.1	858	4	US-09-902-540-3668	Sequence 3668, Ap
C 31	32.8	16.1	1643	4	US-09-902-540-6808	Sequence 6808, Ap
C 32	32.8	16.1	4282	4	US-09-902-540-563	Sequence 563, App
C 33	32.8	16.1	23847	4	US-09-902-540-1177	Sequence 1177, Ap
C 34	32	15.7	807	4	US-09-902-540-6012	Sequence 6012, Ap
C 35	32	15.7	809	4	US-09-902-540-23	Sequence 16667, A
C 36	31.8	15.6	57978	4	US-09-949-016-16667	Sequence 16667, A
C 37	31.6	15.5	1206	4	US-09-902-540-4100	Sequence 1203, Ap
C 38	31.6	15.5	23738	4	US-09-902-540-1203	Sequence 1203, Ap
C 39	31.4	15.4	592	4	US-09-270-767-2308	Sequence 2208, Ap
C 40	31.4	15.4	1980	4	US-09-902-540-9228	Sequence 17590, A
C 41	31.4	15.4	1980	4	US-09-902-540-9228	Sequence 9228, Ap
C 42	31.4	15.4	2007	4	US-09-976-594-407	Sequence 407, App
C 43	31.4	15.4	13234	4	US-09-902-540-986	Sequence 986, App
C 44	31.2	15.3	601	4	US-09-949-016-91879	Sequence 91879, A
C 45	31.2	15.3	601	4	US-09-949-016-194820	Sequence 194820,

## ALIGNMENTS

RESULT 1  
US-08-752-891-1  
Sequence 1, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide



NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-144-178-1

Query Match 100.0%; Score 204; DB 2; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTCTTCGCGTCCCGGCGCCCACTCGCTCCGCTGGCGGAGACGGT 120  
DB 1398 TCTGACGAGGCGCTCTTCGCGTCCCGGCGCCCACTCGCTCCGCTGGCGGAGACGGT 1457  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCATGGC 180  
DB 1458 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCATGGC 1517  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

## RESULT 4

US-09-144-178-5  
Sequence 5, Application US/09144178

Patent No. 5989862

GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko

APPLICANT: NISHIDA, Eisuke

TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/144.178

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752.891

FILING DATE: 20-NOV-1996

APPLICATION NUMBER: JP 8-300856

FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1560 base pairs

TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 30..1541

FEATURE:

NAME/KEY: mat\_peptide

LOCATION: 30..1541

US-09-144-178-5

Query Match 100.0%; Score 204; DB 2; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAGCCGAGCCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 61 TCTGACGAGGCGCTCTTCGCGTCCCGGCGCCCACTCGCTCCGCTGGCGGAGACGGT 120  
DB 1398 TCTGACGAGGCGCTCTTCGCGTCCCGGCGCCCACTCGCTCCGCTGGCGGAGACGGT 1457  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCATGGC 180  
DB 1458 CGTGTGAGCCCTATGTGAGACTTTGCTGATTTTACCGCCCTGTGAGCGTGAACCATGGC 1517  
QY 181 GAGCAGAGCGGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

## RESULT 5

US-09-406-854-1  
Sequence 1, Application US/09406854

Patent No. 6140042

GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko

APPLICANT: NISHIDA, Eisuke

TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/406.854

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/752.891

FILING DATE: 20-NOV-1996

APPLICATION NUMBER: JP 8-300856

FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

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1 SEQUENCE CHARACTERISTICS:
2     LENGTH: 1560 base pairs
3     TYPE: nucleic acid
4     STRANDNESS: double
5     TOPOLOGY: linear
6     FEATURE:
7         NAME/KEY: CDS
8         LOCATION: 30..1541
9     FEATURE:
10        NAME/KEY: mat_peptide
11        LOCATION: 30..1541
12
13 US-09-406854-1

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Query Match	100.0%;	Score 204;	DB 3;	Length 1560;
Best Local Similarity	100.0%;	Pred. No. 3e-48;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CAAAGCCCGACCTTAAACCTCGAAGTCCACCAACACGCAACAGCAGAGCAAGCACTCCACG	60
Db	1338	CAAAGCCCGACCTTAAACCTCGAAGTCCACCAACACGCAACAGCAGAGCAAGCACTCCACG	1397
QY	61	TCGTACGAGAGGCGCTTTCCGCTCCCGGCGCCGCCCACTGCGCTCCGCGTGGAGGAGCGGT	120
Db	1398	TCTACGAGAGGCGCTTTCCGCTCCCGGCGCCGCCCACTGCTCCGCGCTGGAGGAGCGGT	1457
QY	121	CGGTGTGAGCCCTTATGTGTGACCTTTGCTGTGATTTTACCGCGCTCTGAGAGCGTGAACCATATGC	180
Db	1458	CGGTGTGAGCCCTTATGTGTGACCTTTGCTGTGATTTTACCGCGCTCTGAGAGCGTGAACCATATGC	1517
QY	181	GAGCAGAGCGGTGTGACGACGACCG	204
Db	1518	GAGCAGAGCGGTGTGACGACGACCG	1541

RESULT 6  
US-09-406-854-5  
; Sequence 5, Application US/09406854  
; Patent No. 6140040

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? TELEFAX: (202)672-5399
?
? TELEX: 904136
? INFORMATION FOR SEQ ID NO: 5
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1560 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
?
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 30..1541
?
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 30..1541
US-09-406-854-5

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Query Match	100.0%;	Score 204;	DB 3;	Length 1560;
Best Local Similarity	100.0%;	Pred. No. 3e-48;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1338	CAAAGCCGACCTTTAA	CCCTCAGTCCACAA	ACGACACGAGAGGAGAGCTCCAGC	60
Db	1338	CAAAGCCGACCTTTAA <td>CCCTCAGTCCACAA <td>ACGACACGAGAGGAGAGCTCCAGC</td> <td>1397</td> </td>	CCCTCAGTCCACAA <td>ACGACACGAGAGGAGAGCTCCAGC</td> <td>1397</td>	ACGACACGAGAGGAGAGCTCCAGC	1397
QY	61	TCCTGACGAGGCTTTC	CGCTCCCGGCCG	CCGCCACTTCGCTCCGCTGAGCAGACGGT	120
Db	1398	TCCTGACGAGGCTTTC	CGCTCCCGGCCG	CCGCCACTTCGCTCCGCTGAGCAGACGGT	1457
QY	121	CGTGTGAGCCCTTAT	ATGTGAACTTTGCT	GTGAAGTTCACCGCCCTCTGGAGCGTGAACATGAC	180
Db	1458	CGTGTGAGCCCTTAT	ATGTGAACTTTGCT	GTGAAGTTCACCGCCCTCTGGAGCGTGAACATGAC	1517
QY	181	GAGCAGAGCGTGTG	ACAGCACCGC	204	
Db	1518	GAGCAGAGCGTGTG	ACAGCACCGC	1541	

RESULT 7  
US-09-529-279-1  
; Sequence 1, Application US/09529279

Query Match	100.0%;	Score 204;	DB 3;	Length 1560;
Best Local Similarity	100.0%;	Pred. No. 3e-48;		
Matches 204; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 AAAAGCCGACCTTAAACCTCGAGTCAACCAACGACACGACAGCAGCTCCAGC 60  
1338 CAAGGCCGACCTTAAACCTCGAGTCAACCAACGACACGACAGCAGCTCCAGC 1397  
QY 61 TCTGACGAGGACCTTTCCGCTCCGCGCCGCCACTGCGCTCCGCGCTGAGCGAGCGGT 120

Db 1398 TCTGACGAGGAGCTCTTCCCTCCGCGCCGCACTGCTCCGCTGCGAGGAGCGT 1457  
Qy 121 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 180  
Db 1458 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 1517  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1518 GAGCAGAGCGTGTGACAGACCG 1541

## RESULT 8

US-10-158-895-1  
Sequence 1, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-158-895-1

Query Match 100.0%; Score 204; DB 4; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1338 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1397  
Qy 61 TCTGACGAGGAGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGGAGCGT 120  
Db 1398 TCTGACGAGGAGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGGAGCGT 1457  
Qy 121 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 180  
Db 1458 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 1517  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1518 GAGCAGAGCGTGTGACAGACCG 1541

## RESULT 9

US-09-529-279-42  
Sequence 42, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1346 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1405  
Qy 61 TCTGACGAGGAGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGGAGCGT 120  
Db 1406 TCTGACGAGGAGCTCTTCCGCTCCGCGCCGCACTGCTCCGCTGCGAGGAGCGT 1465  
Qy 121 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 180  
Db 1466 CGGTGAGGCGCTATGAGACTTTTACCGGCTTGGAGCGTGAACATGAGC 1525  
Qy 181 GAGCAGAGCGTGTGACAGACCG 204  
Db 1526 GAGCAGAGCGTGTGACAGACCG 1549

## RESULT 10

US-10-158-895-42  
Sequence 42, Application US/10158895  
Patent No. 6551840  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-158-895-42

Query Match 100.0%; Score 204; DB 3; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 3e-48;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 60  
Db 1346 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1405

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QY 61 TCTGACGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGCGGT 120
DB 1406 TCTGACGAGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGCGGT 1465
QY 121 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 180
DB 1466 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 1525
QY 181 GAGCAGAGCGGTGTGACAGACCG 204
DB 1526 GAGCAGAGCGGTGTGACAGACCG 1549

RESULT 11
US-09-529-279-10
; Sequence 10, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 1997-10-22
; PRIOR FILING DATE: 1998-10-22
; PRIOR FILING DATE: 1998-10-22
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-09-529-279-10

Query Match 100.0%; Score 204; DB 3; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACTTCACTGACGACCAACGACGACGACGACGACGACGACG 60
DB 1315 CAAAGCCGACCTTAACTTCACTGACGACCAACGACGACGACGACGACGACGACG 1374
QY 61 TCTGACGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGCGGT 120
DB 1375 TCTGACGAGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGCGGT 1434
QY 121 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 180
DB 1435 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 1494
QY 181 GAGCAGAGCGGTGTGACAGACCG 204
DB 1495 GAGCAGAGCGGTGTGACAGACCG 1518

RESULT 12
US-10-158-895-10
; Sequence 10, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
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; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1557)
US-10-158-895-10

Query Match 100.0%; Score 204; DB 4; Length 1569;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACTTCACTGACGACCAACGACGACGACGACGACGACGACG 60
DB 1315 CAAAGCCGACCTTAACTTCACTGACGACCAACGACGACGACGACGACGACGACG 1374
QY 61 TCTGACGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGAGCGGT 120
DB 1375 TCTGACGAGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGAGCGGT 1434
QY 121 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 180
DB 1435 CGTGTGAGAGCCCTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCATGCG 1494
QY 181 GAGCAGAGCGGTGTGACAGACCG 204
DB 1495 GAGCAGAGCGGTGTGACAGACCG 1518

RESULT 13
US-09-252-991A-4932/C
; Sequence 4932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4932
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4932

Query Match 18.2%; Score 37.2; DB 4; Length 1278;
Best Local Similarity 57.9%; Pred. No. 0.42;
Matches 66; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 64 GACGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGAGCGGT 123
DB 691 GACGAGAGCTCTTCCTCCGCGCCGCCCACTGCTCCCGCTGGCGAGAGAGCGGT 632
QY 124 GTTGAAGCTTATGTGAGACTTTTACCCGCTTGGAGGCTGAGACCAT 177
DB 631 GCCGAGACCGGTCTCGCGCTTGAAGAGAGCGGACGAGTGGCGGCTTAACCTT 578
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 2, 2005, 17:26:02 ; Search time 218.473 Seconds  
(without alignments)  
6043.588 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	204	100.0	US-10-123-427-1	Sequence 1, Appl
2	204	100.0	US-10-123-427-5	Sequence 5, Appl
3	204	100.0	US-10-158-895-1	Sequence 1, Appl
4	204	100.0	US-10-384-743-1	Sequence 1, Appl
5	204	100.0	US-10-158-895-12	Sequence 42, Appl
6	204	100.0	US-10-384-743-42	Sequence 42, Appl
7	204	100.0	US-10-158-895-10	Sequence 10, Appl

8	204	100.0	1569	16	US-10-384-743-10	Sequence 10, Appl
9	204	100.0	3095	20	US-10-820-583A-19	Sequence 19, Appl
10	204	100.0	16877	9	US-09-764-877-3349	Sequence 3349, Ap
11	204	100.0	16877	17	US-10-242-515-3349	Sequence 3349, Ap
12	203.6	99.8	636	9	US-09-925-100-330	Sequence 330, App
13	199.2	97.6	409	10	US-09-918-995-32946	Sequence 32946, A
14	40.4	19.8	1455	18	US-10-425-114-28790	Sequence 28790, A
15	40.4	19.8	1458	18	US-10-425-114-28790	Sequence 28790, A
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20	37.8	18.5	1765	20	US-10-425-115-36243	Sequence 36243, A
21	37.2	18.2	670	17	US-10-264-049-1952	Sequence 1952, Ap
22	36.8	18.0	2036	9	US-09-866-582-17	Sequence 17, Appl
23	36.8	18.0	2036	21	US-10-839-016-17	Sequence 17, Appl
24	36.4	17.8	591	14	US-10-101-464A-289	Sequence 289, App
25	36.4	17.8	591	21	US-10-864-252-289	Sequence 289, App
26	36.4	17.8	2380	14	US-10-101-464A-864	Sequence 864, App
27	36.4	17.8	2380	21	US-10-864-252-864	Sequence 864, App
28	36.2	17.7	2922	15	US-10-156-761-1749	Sequence 1749, Ap
29	36.2	17.7	138203	21	US-10-819-386A-1	Sequence 1, Appl
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39	35.2	17.3	31422	24	US-11-005-196-2	Sequence 2, Appl
40	35	17.2	535	17	US-10-437-963-21851	Sequence 21851, A
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43	35	17.2	1785	20	US-10-739-930-2060	Sequence 2060, Ap
44	35	17.2	5811	13	US-10-002-600-15	Sequence 15, Appl
45	34.8	17.1	459	20	US-10-425-115-22523	Sequence 22523, A

## ALIGNMENTS

RESULT 1  
US-10-123-427-1  
; Sequence 1, Application US/10123427  
; Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996

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1  APPLICATION NUMBER: JP 8-300856
2  FILING DATE: 28-OCT-1996
3  APPLICATION NUMBER: JP 8-126282
4  FILING DATE: 24-APR-1996
5
6  ATTORNEY/AGENT INFORMATION:
7  NAME: BENT, Stephen A.
8  REGISTRATION NUMBER: 29,768
9  REFERENCE/DOCKET NUMBER: 17981/1111
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (202)672-5530
12 TELEFAX: (202)672-5399
13
14 TELEX: 904136
15
16 INFORMATION FOR SEQ ID NO: 1:
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18   SEQUENCE CHARACTERISTICS:
19     LENGTH: 1560 base pairs
20     TYPE: nucleic acid
21     STRANDEDNESS: double
22     TOPOLOGY: linear
23
24   FEATURE:
25     NAME/KEY: CDS
26     LOCATION: 30..1541
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28   FEATURE:
29     NAME/KEY: mat_peptide
30     LOCATION: 30..1541
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Best Local Similarity	100.0%	Pred. No.	6, 2e-53	
Matches 204; Conservative	0	Mismatches	0	Gaps 0

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Db	1338	CAAAAGCCGACCTTAACCTTCGAGTCCACCAACGACACGCAAGCAGACGCTCCAGC	1397
QY	61	TCTGACGAGGAGCTCTTCCGCTCCCGGCGCGCCCACTGAGCTCCGCGCTGGGAGGACGGT	120
Db	1398	TCTACCGAGGAGCTCTTCCGCTCCCGGCGCGCCCACTGAGCTCCGCGCTGGGAGGACGGT	1457
QY	121	CGTGTGAGCCCTAATGTGACCTTTGCTGAGTTTAAACGACTGTGAGCGTGAACCATAGC	180
Db	1458	CGTGTGAGCCCTAATGTGACCTTTGCTGAGTTTAAACGACTGTGAGCGTGAACCATAGC	1517
QY	181	GAGCAGAGCGCTGTGACAGCACCG	204
Db	1518	GAGCAGAGCGCTGTGACAGCACCG	1541

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1      RESULT 2
2      US-10-123-427-5
3      / Sequence 5, Application US/10123427
4      / Publication No. US20020119525A1
5      /
6      / GENERAL INFORMATION:
7      /
8      / APPLICANT: MATSUMOTO, Kunihiko
9      / NISHIDA, Eisuke
10     /
11     / TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR
12     /
13     / NUMBER OF SEQUENCES: 8
14     /
15     / CORRESPONDENCE ADDRESS:
16     / ADDRESS: Foley & Lardner
17     / STREET: 3000 K Street, N.W., Suite 500
18     / CITY: Washington
19     /
20     / STATE: D. C.
21     /
22     / COUNTRY: USA
23     /
24     / ZIP: 20007-5109
25     /
26     / COMPUTER READABLE FORM:
27     /
28     / MEDIUM TYPE: Floppy disk
29     /
30     / COMPUTER: IBM PC compatible
31     /
32     / OPERATING SYSTEM: PC-DOS/MS-DOS
33     /
34     / SOFTWARE: Patentin Release #1.0, Version #1.30
35     /
36     / CURRENT APPLICATION DATA:
37     /
38     / APPLICATION NUMBER: US/10/123,427
39     /
40     / FILING DATE: 17-Apr-2002
41     /
42     / CLASSIFICATION: <Unknown>

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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: US/09/406,854
3      FILING DATE: <unknown>
4      APPLICATION NUMBER: US/08/752,891
5      FILING DATE: 20-NOV-1996
6      APPLICATION NUMBER: JP 8-300856
7      FILING DATE: 28-OCT-1996
8      APPLICATION NUMBER: JP 8-126282
9      FILING DATE: 24-APR-1996
10     ATTORNEY/AGENT INFORMATION:
11     NAME: BENT, Stephen A.
12     REGISTRATION NUMBER: 29,768
13     REFERENCE/DOCKET NUMBER: 17981/11111
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: (202)672-5300
16     TELEFAX: (202)672-5399
17     TELER: 904136
18     INFORMATION FOR SEQ ID NO: 5:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH: 1560 base pairs
21     TYPE: nucleic acid
22     STRANDEDNESS: double
23     TOPOLOGY: linear
24     FEATURE:
25     NAME/KEY: CDS
26     LOCATION: 30..1541
27     FEATURE:
28     NAME/KEY: mat_peptide
29     LOCATION: 30..1541
30     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
31     US-10-123-427-5

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SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-123-427-5

Query Match	100.0%	Score 204	DB 13	Length 1560	
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				Gaps	0
QY	1	CAAAAGCCCGACCTTAACTCCGAGTCACCAACGACACGACGACGAGCAGCAGCTCCAGC	60		
Db	1338	CAAAAGCCCGACCTTAACTCCGAGTCACCAACGACACGACGACGAGCAGCTCCAGC	139		
QY	61	TCTGACGAGGAGCTCTTCCGCTCCCGGCGGCGCCACTGCGTCCCGCTGGGAGGACCGT	120		
Db	1398	TCTGACGAGGAGCTCTTCCGCTCCCGGCGGCGCCACTGCGTCCCGCTGGGAGGACCGT	145		
QY	121	CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTAAACGCTCTGTGAGCGTGAACCATGAC	180		
Db	1458	CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTAAACGCTCTGTGAGCGTGAACCATGAC	151		
QY	181	GAGCAGAGCGGTGTGACAGACACCG	204		
Db	1518	GAGCAGAGCGGTGTGACAGACACCG	1541		

RESULT 3  
 US-10-158-895-1  
 Sequence 1, Application US/10158895  
 Publication No. US20020155624A1  
 GENERAL INFORMATION:  
 APPLICANT: ONO, KOICHIRO  
 APPLICANT: OHTOMO, TOSHIHIKO  
 APPLICANT: TSUCHIYA, MASAYUKI  
 TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
 FILE REFERENCE: 053466/0218  
 CURRENT APPLICATION NUMBER: US/10/158, 895  
 CURRENT FILING DATE: 2002-06-03  
 PRIOR APPLICATION NUMBER: US/09/529, 279  
 PRIOR FILING DATE: 2000-04-11  
 PRIOR APPLICATION NUMBER: PCT/JP98/04796  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: JP 9/290188  
 PRIOR FILING DATE: 1997-10-22  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-158-895-1

Query Match 100.0%; Score 204; DB 13; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
DB 1338 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 1337  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 120  
DB 1398 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 1457  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 180  
DB 1458 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 1517  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

RESULT 4  
US-10-384-743-1  
Sequence 1, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1560  
TYPE: DNA  
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1541)  
US-10-384-743-1

Query Match 100.0%; Score 204; DB 16; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
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QY 61 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 120  
DB 1398 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 1457  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 180

DB 1458 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 1517  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 1518 GAGCAGAGCGTGTGACGACGACCG 1541

RESULT 5  
US-10-158-895-42  
Sequence 42, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-158-895-42

Query Match 100.0%; Score 204; DB 13; Length 1568;  
Best Local Similarity 100.0%; Pred. No. 6.2e-53;  
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QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 60  
DB 1346 CAAAGCCGACCTTAACCTTCAGTCCAGCAACGACGACGACGACGACGCTCCAGC 1405  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 120  
DB 1406 TCTGACGAGAGGCTCTTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGAGAGCGT 1465  
QY 121 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 180  
DB 1466 CGTGTGAGCCCTTAATGAGACTTTGAGTTTAAACGCTCTGAGAGGTGACCATGCG 1525  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 1526 GAGCAGAGCGTGTGACGACGACCG 1549

RESULT 6  
US-10-384-743-42  
Sequence 42, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22



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; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 19
; LENGTH: 3095
; TYPE: DNA
; ORGANISM: HUMAN
US-10-820-583A-19

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Query Match	100.0%;	Score 204;	DB 20;	Length 3095;
Best Local Similarity	100.0%;	Pred. No. 6.4e-53;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	CAAGGCCGCACTTAACTTCGAGTCAACAAGCAACGCAAGGAGGAGCTCCAGC	60
Db	1329	CAAGCCCGACCTTAACTTCGAGTCAACAAGCAACGCAAGGAGGAGCTCCAGC	1388
QY	61	TCTGACGAGAGGCTCTTCGCGTCCCGGACCGGCCACTGCGTCCGCGTGGCGAGGACGGT	120
Db	1389	TCTGACGAGAGGCTCTTCGCGTCCCGGACCGGCCACTGCGTCCGCGTGGCGAGGACGGT	1448
QY	121	CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGGCTGACCATGGC	180
Db	1449	CGTGTGAGCCCTATGTGACCTTTGCTGAGTTTACCGCTCTGGAGGCTGACCATGGC	1508
QY	181	GAGCAGAGCGTGTGACAGCACCG	204
Db	1509	GAGCAGAGCGTGTGACAGCACCG	1532

RESULT 10  
US-09-764-877-3349  
; Sequence 3349, Application US/09764877

Query Match	100.0%;	Score 204;	DB 9;	Length 16877;
Best Local Similarity	100.0%;	Pred. No. 6.8e-53;		
Matches 204; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	CAAAAGCCCGACCTTAAACCTTCGACATCCACCAACAAGACACGACAGACACCTCCAGC	60
Db	15011	CAAAAGCCCGACCTTAAACCTTCGACATCCACCAACAAGACACGACAGACACCTCCAGC	15070
QY	61	TCGTACGAGAGGCGCTCTTCCGCTCCCGGCGCCGACCTCGCTCCCGCTGTGCGAGGACG	120
Db	15071	TCGTACGAGAGGCGCTCTTCCGCTCCCGGCGCCGACCTCGCTCCCGCTGTGCGAGGACG	15130
QY	121	CGTGTGTGAGCCCTATGTGAGACTTTTGCTGATTTTAAACGCGCTCTGAGACGTGACCAATGCG	180
Db	15131	CGTGTGTGAGCCCTATGTGAGACTTTTGCTGATTTTAAACGCGCTCTGAGACGTGACCAATGCG	15190
QY	181	GAGCAGAGCGCTGTGTGACGACACCG	204
Db	15191	GAGCAGAGCGCTGTGTGACGACACCG	15214

RESULT 11  
US-10-242-515-3349  
; Sequence 3349, Application US/10242515

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Publication No. US20040009488A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
PRIORITY FILING DATE: 2002-09-13
PRIORITY APPLICATION NUMBER: 09/764,877
PRIORITY FILING DATE: 2001-01-17
PRIORITY APPLICATION NUMBER: 60/179,065
PRIORITY FILING DATE: 2000-01-31
PRIORITY APPLICATION NUMBER: 60/180,628
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: 60/214,886
PRIORITY FILING DATE: 2000-06-28
PRIORITY APPLICATION NUMBER: 60/217,487
PRIORITY FILING DATE: 2000-07-11
PRIORITY APPLICATION NUMBER: 60/225,758
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/220,963
PRIORITY FILING DATE: 2000-07-26
PRIORITY APPLICATION NUMBER: 60/217,496
PRIORITY FILING DATE: 2000-07-11
PRIORITY APPLICATION NUMBER: 60/225,447
PRIORITY FILING DATE: 2000-08-14
PRIORITY APPLICATION NUMBER: 60/218,290
PRIORITY FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3349
LENGTH: 16877
TYPE: DNA
ORGANISM: Homo sapiens
US-10-242-515-3349

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Query Match	100.0%;	Score 204;	DB 17;	Length 16877;
Best Local Similarity	100.0%;	Pred. No. 6.8e-53;		
Matches 204; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	CAAAGCCCGACCTTAAACCCGAGAGTCCACCAACGACACCGAGAGGACAGCTCCACG	60
Db	15011	CAAAGCCCGACCTTAAACCCGAGAGTCCACCAACGACACCGAGAGGACAGCTCCACG	15077
QY	61	TCTGACGAGAGGCTCTTCCGCTCCGGCCGACCACACTCGCTCCCGCTTGAGCAGACGGT	120
Db	15071	TCTGACGAGAGGCTCTTCCGCTCCGGCCGACCACACTCGCTCCCGCTTGAGCAGACGGT	15130
QY	121	CGGTGTAGGCCCTATGTGTGAATTTCCTGAGTTTACCGGCTCTGGAGCGTGAACATGGC	180
Db	15131	CGGTGTAGGCCCTATGTGTGAATTTCCTGAGTTTACCGGCTCTGGAGCGTGAACATGGC	15190
QY	181	GAGCAGAGCGGTGTGAAGACACCG	204
Db	15191	GAGCAGAGCGGTGTGAAGACACCG	15214

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RESULT 12
US-09-925-300-330
; Sequence 330, Application US/09925300
; Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruden
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890

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Query Match 19.8%; Score 40.4; DB 18; Length 1458;  
Best Local Similarity 55.7%; Pred. No. 0.013; Indels 1; Gaps 1;  
Matches 97; Conservative 0; Mismatches 76;  
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Db 1093 GCCGTCCGCGCTGAAAGCTCTGCAAGCAGCGCCGCTCGCTCCG-CGAACTCTCTCCG 1035  
QY 81 CTCCCGGCCGCCCACTCGCTCCCGCTGCGGAGACGCTGCTTGAACCTTATGGA 140  
Db 1034 CCGTCCGCCGCCGCCGCCGCTGACTAAGCGCGCGAAAGGCGCTGTGAGTCAAGAGGA 975  
QY 141 CTTGCTGAGTTTAAACGCTCTGAGGCTGACCATGCGAGCAGAGCGTGT 134  
Db 974 GGAAGTACGGTTGCGCGGTCGAGCGCGGACGACCTGAGCGCGCGT 921

Search completed: August 2, 2005, 20:15:29  
Job time : 223.473 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus.n2p model

Run on: August 2, 2005, 17:28:02 ; Search time 6.66216 Seconds  
(without alignments)  
4571.612 Million cell updates/sec

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Sequence: 1 caaagccgcagccttaacct.....agaagctgtgtgacagcacccg 204

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aa/PCTUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	359	99.4	504	2	US-08-752-891-6
3	359	99.4	504	2	US-09-144-178-2
4	359	99.4	504	2	US-09-144-178-6
5	359	99.4	504	3	US-09-406-854-2
6	359	99.4	504	3	US-09-406-854-6
7	359	99.4	504	4	US-09-529-279-2
8	359	99.4	504	4	US-10-158-895-2
9	359	99.4	513	4	US-09-529-279-43
10	359	99.4	513	4	US-10-158-895-43
11	359	99.4	517	4	US-09-529-279-11
12	359	99.4	517	4	US-10-158-895-11

13	100.5	27.8	136	4	US-09-252-991A-22734	Sequence 22734, A
C 14	92.5	24.6	189	4	US-09-252-991A-17056	Sequence 17056, A
C 15	89.5	23.8	1303	4	US-09-252-991A-19799	Sequence 19799, A
C 16	86.5	23.0	466	4	US-09-252-991A-22592	Sequence 22592, A
C 17	84.5	22.5	363	4	US-09-252-991A-20195	Sequence 20195, A
C 18	84	22.3	333	4	US-09-252-991A-20478	Sequence 20478, A
C 19	84	22.3	721	4	US-09-252-991A-28293	Sequence 28293, A
C 20	83.5	22.2	338	4	US-09-252-991A-16820	Sequence 16820, A
C 21	83.5	22.2	480	4	US-09-252-991A-20125	Sequence 20125, A
C 22	83	22.1	264	4	US-09-252-991A-24262	Sequence 24262, A
C 23	82	21.8	269	4	US-09-252-991A-26605	Sequence 26605, A
C 24	81.5	21.7	200	4	US-09-252-991A-19793	Sequence 19793, A
C 25	81.5	21.7	355	4	US-09-252-991A-22326	Sequence 22326, A
C 26	81	21.5	201	4	US-09-252-991A-25745	Sequence 25745, A
C 27	81	21.5	1228	4	US-09-252-991A-17764	Sequence 17764, A
C 28	80.5	21.4	239	4	US-09-252-991A-25387	Sequence 25387, A
C 29	80.5	21.4	589	4	US-09-252-991A-32631	Sequence 32631, A
C 30	80	21.3	338	4	US-09-252-991A-19609	Sequence 19609, A
C 31	79.5	22.0	136	4	US-09-252-991A-23572	Sequence 23572, A
C 32	79	21.0	243	4	US-09-252-991A-26015	Sequence 26015, A
C 33	79	21.0	350	4	US-09-252-991A-19537	Sequence 19537, A
C 34	78.5	20.9	268	4	US-09-252-991A-27950	Sequence 27950, A
C 35	78.5	20.9	297	4	US-09-252-991A-18932	Sequence 18932, A
C 36	78	20.7	416	4	US-09-252-991A-32875	Sequence 32875, A
C 37	78	20.7	710	4	US-09-252-991A-24946	Sequence 24946, A
C 38	77.5	20.6	246	4	US-09-252-991A-23345	Sequence 23345, A
C 39	77.5	20.6	345	4	US-09-252-991A-32325	Sequence 32325, A
C 40	77	21.3	16	4	US-09-529-279-41	Sequence 41, Appl
C 41	77	21.3	16	4	US-10-158-895-41	Sequence 41, Appl
C 42	77	20.5	279	4	US-09-252-991A-26860	Sequence 26860, A
C 43	77	20.5	586	4	US-09-252-991A-28601	Sequence 28601, A
C 44	77	20.5	763	4	US-09-252-991A-30146	Sequence 30146, A
C 45	76.5	21.2	224	4	US-09-252-991A-19251	Sequence 19251, A

## ALIGNMENTS

RESULT 1  
US-08-752-891-2  
Sequence 2, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:



REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-144-178-2

Alignment Scores:  
Pred. No.: 4.49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 2 Gaps: 0

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QY 1 CAAGCCCGACCTTAACCTTCAGTCCAGCAACAGCAGCAGCAGCAGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGAGCCTCTTCCTCCGCTCCGCGCCGCCACTGCTCCGCTGCGCAGACCGT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProIahIstSerLeuProGlyGluAspIly 476  
QY 121 CGGTGAGCCCTATGTGACCTTGCTGAGTTTACCGCCCTCTGAGAGGTGACCATGCG 180  
DB 477 ArgValGluProTyrValAspPheIahGluPheTyrArgLeuTyrSerValAspIstIly 496  
QY 181 GAGCAGAGCGGTGTGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 4  
US-09-144-178-6  
Sequence 6, Application US/09144178  
Patent No. 589862  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144.178  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-144-178-6

Alignment Scores:  
Pred. No.: 4.49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 2 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-09-144-178-6 (1-504)

QY 1 CAAGCCCGACCTTAACCTTCAGTCCAGCAACAGCAGCAGCAGCAGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGAGCCTCTTCCTCCGCTCCGCGCCGCCACTGCTCCGCTGCGCAGACCGT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProIahIstSerLeuProGlyGluAspIly 476  
QY 121 CGGTGAGCCCTATGTGACCTTGCTGAGTTTACCGCCCTCTGAGAGGTGACCATGCG 180  
DB 477 ArgValGluProTyrValAspPheIahGluPheTyrArgLeuTyrSerValAspIstIly 496  
QY 181 GAGCAGAGCGGTGTGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 5  
US-09-406-854-2  
Sequence 2, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406.854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282

FILED DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-2

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 3 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-09-406-854-2 (1-504)

QY 1 CAAAGCCCGACCTTAACTTCAGTCCACGACGACGACGACGACGACGCTCCAGC 60  
Db 437 GlnSerProThrLeuThrLeuGlnSerThrAnthrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGAGGCTCTTCCGCTCCCGGCGCCGACCTGCTCCCGCTGCGAGAGCGGT 120  
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGAGACTTTGCTGAGTTTACCGCTCTGAGCGTGAACATGCG 180  
Db 477 ArgValGluProTyValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGGAGAGCGGTGAGACGACGACG 204  
Db 497 GluGlnSerValValThrAlaPro 504

RESULT 6  
US-09-406-854-6  
Sequence 6, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-6

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 3 Gaps: 0

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Db 437 GlnSerProThrLeuThrLeuGlnSerThrAnthrHisThrGlnSerSerSerSer 456  
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Db 497 GluGlnSerValValThrAlaPro 504

RESULT 7  
US-09-529-279-2  
Sequence 2, Application US/09529279  
Patent No. 6451617  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIOKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/09/529,279  
CURRENT FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-529-279-2

Alignment Scores:  
Pred. No.: 4,49e-34 Length: 504  
Score: 359.00 Matches: 68  
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

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Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
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QY 61 TCTGACGAGGCGCTTCCTCCGCTCCCGGCGCCCACTGCTCCCGCTCCGCTGGGAGAGCGGT 120
DB 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485
QY 121 CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGACGATGAGC 180
DB 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrPserValAspHisGly 505
QY 181 GAGCAGAGCGCTGTGACGACGACCG 204
DB 506 GluGlnSerValValThrAlaPro 513

RESULT 11
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0276
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-11

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Pred. No.: 4,51e-34 Length: 517
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DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
QY 121 CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGACGATGAGC 180
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrPserValAspHisGly 496
QY 181 GAGCAGAGCGCTGTGACGACGACCG 204
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RESULT 12
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0276
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
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; ORGANISM: Homo sapiens
US-10-158-895-11

Alignment Scores:
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DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476
QY 121 CGTGTGAGCCCTAATGTGACTTTGCTGAGTTTACCGCTCTGAGCGTGACGATGAGC 180
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrPserValAspHisGly 496
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DB 497 GluGlnSerValValThrAlaPro 504

RESULT 13
US-09-252-991A-22734
; Sequence 22734, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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2	359	99.4	504	US-10-123-427-6	Sequence 6, Appl1
3	359	99.4	504	US-10-158-895-2	Sequence 2, Appl1
4	359	99.4	504	US-10-184-743-2	Sequence 2, Appl1
5	359	99.4	504	US-10-820-583A-10	Sequence 10, Appl1
6	359	99.4	513	US-10-158-895-43	Sequence 43, Appl1
7	359	99.4	513	US-10-384-743-43	Sequence 43, Appl1
8	359	99.4	517	US-10-158-895-11	Sequence 11, Appl1
9	359	99.4	517	US-10-384-743-11	Sequence 11, Appl1
10	352	97.5	84	US-09-925-300-1270	Sequence 8, Appl1
11	96.5	25.7	19608	US-10-084-846A-8	Sequence 8, Appl1
12	89.5	24.8	215	US-10-425-115-347124	Sequence 347124, A
13	87	23.1	245	US-10-282-122A-62088	Sequence 62088, A
14	86	22.9	588	US-10-437-963-121108	Sequence 121108, A
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16	85	23.5	274	US-10-425-115-293205	Sequence 293205, A
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25	80.5	21.4	291	US-10-425-114-68835	Sequence 68835, A
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32	78	21.6	96	US-10-437-963-141575	Sequence 141575, A
33	78	21.6	131	US-10-437-963-111977	Sequence 111977, A
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35	77.5	20.6	359	US-10-479-571-1	Sequence 1, Appl1
36	77.5	20.6	509	US-10-437-963-117352	Sequence 117352, A
37	77	21.3	16	US-10-158-895-41	Sequence 41, Appl1
38	77	21.3	16	US-10-384-743-41	Sequence 41, Appl1
39	77	20.5	113	US-10-437-963-153139	Sequence 153139, A
40	77	21.3	154	US-10-437-963-115596	Sequence 115596, A
41	77	21.3	164	US-10-437-963-115597	Sequence 115597, A
42	77	20.5	230	US-10-424-599-272218	Sequence 272218, A
43	76.5	21.2	113	US-10-084-846A-5	Sequence 5, Appl1
44	76.5	21.2	113	US-10-425-115-275619	Sequence 275619, A
45	76.5	20.3	230	US-10-437-963-204430	Sequence 204430, A

#### ALIGNMENTS

RESULT 1  
US-10-123-427-2

; Sequence 2, Application US/10123427  
; Publication No. US20020119525A1

; GENERAL INFORMATION:

APPLICANT: MATSUMOTO, Kunihiko  
NISHIDA, Eisuke

TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-APR-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-123-427-2  
  
Alignment Scores:  
Pred. No.: 4,15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
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QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGCGCTCTCCGCTCCCGGCGCCGACGCTCCGCTCCGCTCCGCGAGCGGT 120  
DB 457 SerAspGlyIleuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
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US-10-123-427-6  
Sequence 6, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-APR-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
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DB 477 ArgValGluProTyrValaIapPheAlaGluPheTyrArgLeuTyrPserValaIapHisGly 496  
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DB 497 GluGlnSerValValThrAlaPro 504  
  
RESULT 3  
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Sequence 2, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
OHOMO, TOSHITAKA  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-2

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 99.45% Indels: 0  
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QY 61 TCTGACGAGAGCCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTCGGAGAGCGGT 120  
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Sequence 2, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-2

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 14 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-2 (1-504)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGAGCCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTCGGAGAGCGGT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGGTGAGCCCTATGTGACTTTGCTGATTTTACCCCTCTGAGGCTGACCATGGC 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 5  
US-10-820-583A-10  
Sequence 10, Application US/10820583A  
Publication No. US20040242461A1  
GENERAL INFORMATION:  
APPLICANT: Schneider, Michael  
APPLICANT: Oh, Hidemasa  
TITLE OF INVENTION: Modulators of Telomere Stability  
FILE REFERENCE: HO-P02673US1  
CURRENT APPLICATION NUMBER: US/10/820,583A  
CURRENT FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 60/461,095  
PRIOR FILING DATE: 2003-04-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 504  
TYPE: PRT  
ORGANISM: HUMAN  
US-10-820-583A-10

Alignment Scores:  
Pred. No.: 4.15e-30 Length: 504  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 16 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-820-583A-10 (1-504)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 456  
QY 61 TCTGACGAGAGCCTCTTCGCTCCGCGCCGCCCACTGCTCCGCTCGGAGAGCGGT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGGTGAGCCCTATGTGACTTTGCTGATTTTACCCCTCTGAGGCTGACCATGGC 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 497 GluGlnSerValValThrAlaPro 504

RESULT 6  
US-10-158-895-43  
Sequence 43, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO

APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-43

Alignment Scores:  
Pred. No.: 4.16e-30 Length: 513  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-158-895-43 (1-513)

QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 60  
DB 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 465  
QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGACGCT 120  
DB 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485  
QY 121 CGTGTGAGCCCTATGTGACTTTGCTGAGTTTACCGCTCGAGACGCTGACCATGCG 180  
DB 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 505  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 506 GluGlnSerValValThrAlaPro 513

RESULT 7

US-10-384-743-43  
Sequence 43, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-43

Alignment Scores: 4.16e-30 Length: 513  
Pred. No.: 4.16e-30 Length: 513

Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 14 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-43 (1-513)

QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 60  
DB 446 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 465  
QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGACGCT 120  
DB 466 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 485  
QY 121 CGTGTGAGCCCTATGTGACTTTGCTGAGTTTACCGCTCGAGACGCTGACCATGCG 180  
DB 486 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 505  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204  
DB 506 GluGlnSerValValThrAlaPro 513

RESULT 8

US-10-158-895-11  
Sequence 11, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-11

Alignment Scores:  
Pred. No.: 4.16e-30 Length: 517  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.45% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-158-895-11 (1-517)

QY 1 CAAGCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 60  
DB 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGCTCTTCCTCCGCTCCGCGCCGACCTGCTCCGCTGCGAGACGCT 120  
DB 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTGACTTTGCTGAGTTTACCGCTCGAGACGCTGACCATGCG 180  
DB 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACGACGACCG 204

Db 497 GluGlnSerValValThrAlaPro 504

## RESULT 9

US-10-384-743-11  
Sequence 11, Application US/10384743  
Publication No. US2003016228A1

## GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 517  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-11

## Alignment Scores:

Pred. No.:	4,16e-30	Length:	517
Score:	359.00	Matches:	68
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.45%	Indels:	0
DB:	14	Gaps:	0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-384-743-11 (1-517)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACAGCAGCAGCAGCAGCAGCTCCAGC 60  
Db 437 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 456  
QY 61 TCTGACGAGGCTCTTCCGCTCCCGCCGCCCACTGCTCCCGCTGGGAGAGACGT 120  
Db 457 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 476  
QY 121 CGTGTGAGCCCTATGTCGACTTTCGAGTTTACCGCCCTCTGAGGCGTGGACCATGCG 180  
Db 477 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 496  
QY 181 GAGCAGAGCGTGTGACAGCAGCCG 204  
Db 497 GluGlnSerValValThrAlaPro 504

## RESULT 10

US-09-925-300-1270  
Sequence 1270, Application US/09925300  
Patent No. US2002015168A1  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
APPLICANT: Steve Ruben,  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA101  
CURRENT APPLICATION NUMBER: US/09/925,300  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1270

LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (38)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1270

## Alignment Scores:

Pred. No.:	1.97e-29	Length:	84
Score:	352.00	Matches:	67
Percent Similarity:	98.53%	Conservative:	0
Best Local Similarity:	98.53%	Mismatches:	1
Query Match:	97.51%	Indels:	0
DB:	9	Gaps:	0

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-09-925-300-1270 (1-84)

QY 1 CAAAGCCGACCTTAACCTTCAGTCCAGCAACAGCAGCAGCAGCAGCAGCTCCAGC 60  
Db 17 GlnSerProThrLeuThrLeuGlnSerThrAsnThrIsthrGlnSerSerSerSer 36  
QY 61 TCTGACGAGGCTCTTCCGCTCCCGCCGCCCACTGCTCCCGCTGGGAGAGACGT 120  
Db 37 Ser\*\*\*GlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 56  
QY 121 CGTGTGAGCCCTATGTCGACTTTCGAGTTTACCGCCCTCTGAGGCGTGGACCATGCG 180  
Db 57 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 76  
QY 181 GAGCAGAGCGTGTGACAGCAGCCG 204  
Db 77 GluGlnSerValValThrAlaPro 84

## RESULT 11

US-10-084-846A-8

Sequence 8, Application US/10084846A  
Publication No. US20040006026A1  
GENERAL INFORMATION:  
APPLICANT: WEITNAUER, GABRIELE  
APPLICANT: MOHLENWEG, AGNES  
APPLICANT: TREPZER, AXEL  
APPLICANT: BECHTOLD, ANDREAS  
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES  
FILE REFERENCE: 1974-005  
CURRENT APPLICATION NUMBER: US/10/084,846A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: PCT/EP01/09815  
PRIOR FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: DE 101 09 166.4  
PRIOR FILING DATE: 2001-02-25  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 8

## LENGTH: 19608

## TYPE: PRT

ORGANISM: Streptomyces viridochromogenes

## FEATURE:

OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.

US-10-084-846A-8

## Alignment Scores:

Pred. No.:	0.179	Length:	19608
Score:	96.50	Matches:	28
Percent Similarity:	46.34%	Conservative:	10
Best Local Similarity:	34.15%	Mismatches:	21
Query Match:	25.66%	Indels:	23
DB:	15	Gaps:	5

US-09-830-144-3\_COPY\_1338\_1541 (1-204) x US-10-084-846A-8 (1-19608)

```

QY      190  CCTCTGCTGCAGCTCCAGCTCCAGA-----GGCGGAAA 152
           ||:::  ||:::|||||  |||
Db      16705  ArgAlaAsnArgAsnGlyProArgArgArgTrpArgArgCysIleuSerProAlaGlyArg 16724
           ||:::  ||:::|||||  |||

QY      151  ACTGACGAAGTCCACATMGGCTCAACAGACCTGCT-----CGC 110
           ||:::  ||:::|||||  |||
Db      16725  ThrArgSerSerProAspArgArgGlnIgluArgProGlyCysCysAlaGlySerArg 16744
           ||:::  ||:::|||||  |||

QY      109  CAGCGCGAGACGATGGCGGGCGGGAGCGGAAGAGCGCTCCGTACAGACTGGAAGCTGC 50
           |||||  ||::  ||:::|||||  |||
Db      16745  ProAlaGlyGlyAlaArgAsnGlyGluAlaGlyArgAlaArgArgArg---ArgCys 16763
           |||||  ||::  ||:::|||||  |||

QY      49  -----TGCCTGCGTGTGCGGT-----TGCTGACTGCAGAG 17
           |||||  |||||  |||
Db      16764  GlyArgGlyProProAlaProCysSerProCysProCysProMetPheGlnThrProGly 16783
           |||||  |||||  |||

QY      16  TTAAG 11
           |||
Db      16784  ArgArg 16785

RESULT 12
US-10-425-115-347124
; Sequence 347124, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 347124
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; ; OTHER INFORMATION: Clone ID: MRP4577_79741C.1.pep
US-10-425-115-347124

Alignment Scores:
Pred. No.:      0.638      Length:      215
Score:          89.50      Matches:      24
Percent Similarity: 45.45%      Conservative: 6
Best Local Similarity: 36.36%      Mismatches: 27
Query Match:      24.79%      Indels:      9
DB:               16      Gaps:      2

US-09-830-144-3_COPY_1338_1541 (1-204) x US-10-425-115-347124 (1-215)

QY      2  AAAGCCGACCTTAAACCTGTGAGTCA-----CCAACAGCAGACAGCAGAGCAGA 52
           ::::  |||||  |||
Db      100  ArgProArgProThrProThrProProIleuSerSerProThrArgArgThrArgTrpTrp 119
           ::::  |||||  |||

QY      53  GCTCAGGCTGAGCGAGAGCCCTCTCCGCTCCCGGCGCGGCCACACTGCTCCGCCCTGAGCG 112.
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      120  ProProArgSerThrArgCysSerProSerProProProProProArgAla----- 136
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      113  AGAAGCGTGTGTTGAGCCCTATGTGACCTTTGCTGAGTTTAAAGCCTCTGAGAGGTGG 172
           ::::  |||||  |||  |||  |||  |||  |||  |||  |||  |||
Db      137  -----IleIeuSerProThrProThrProThrThrAlaSerMetSerSerThrCysTrp 153
           ::::  |||||  |||  |||  |||  |||  |||  |||  |||  |||

QY      173  ACCATGCGAGCAGACGCG 190
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      154  ThrArgThrProArgAla 159
           |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 13
US-10-282-122A-62088
; Sequence 62088, Application US/10282122A
; Publication No. US20040029129A1

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/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zykkind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: EMTTRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 62088
/ LENGTH: 245
/ TYPE: PRT
/ ORGANISM: Mycobacterium avium
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (80)..(80)
/ OTHER INFORMATION: X=any amino acid
US-10-282-122A-62088

Alignment Scores:
Pred. No.: 1,21 Length: 245
Score: 87.00 Matches: 29
Percent Similarity: 41.46% Conservative: 5
Best Local Similarity: 35.37% Mismatches: 30
Query Match: 23.14% Indels: 18
DB: 15 Gaps: 5

US-09-830-144-3_COPY_1338_1541 (1-204) x US-10-282-122A-62088 (1-245)
QY 196 TCACACAGCTCT-----GCTCGCATTGTCACAGCTCCAGAGGC 158
D 101 SerProArgSerThrProArgProProthThrThrSerProthProArgSerThrSer 120
QY 157 -----GTTAAACTCAGCAAGTCCAAATGGGGCTCAACACGACCGTCTCGCAGGCG 104
D 121 TrpIleAlaSerThrThaArgSerProArgArgSerGlyProAlaIhrProArgProSer 140
QY 103 GGAGCGAGTGGGCGGGCGGAGCGGAGAGAGGCTCCGT-----CAGAGCTGG 56
D 141 ArgAlaSerSerSerIleAlaSerThrThrArgProAlaIaAlaGlySerSerTrp 160
QY 55 -----AGTGTCTGC-----TCTGCGTGTGCGGTGTGGAGACTGACAGGTTAAG 11

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2005, 20:15:38 ; Search time 8.27027 Seconds  
(without alignments)  
613.781 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359 1 QSTPLTQSTNTHTQSSSSS.....AEFYRLMSVDHGQSVYTPA 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	504	2	US-08-752-891-2
2	359	100.0	504	2	US-08-752-891-6
3	359	100.0	504	2	US-09-144-178-2
4	359	100.0	504	2	US-09-144-178-6
5	359	100.0	504	3	US-09-406-854-2
6	359	100.0	504	3	US-09-406-854-6
7	359	100.0	504	4	US-09-529-279-2
8	359	100.0	504	4	US-10-158-895-2
9	359	100.0	513	4	US-09-529-279-43
10	359	100.0	513	4	US-10-158-895-43
11	359	100.0	517	4	US-09-529-279-11
12	359	100.0	517	4	US-10-158-895-11
13	77	21.4	16	4	US-09-529-279-40
14	77	21.4	16	4	US-10-158-895-41
15	75.5	21.0	691	4	US-09-902-540-16476
16	67.5	18.8	752	4	US-09-919-039-235
17	67.5	18.8	852	2	US-09-070-060-3
18	67.5	18.8	852	2	US-09-357-746-3
19	66.5	18.5	425	4	US-09-248-796A-14511
20	66.5	18.4	16	4	US-09-529-279-40
21	66	18.4	16	4	US-10-158-895-40
22	65.5	18.2	498	4	US-10-037-667-5
23	65	18.1	335	4	US-09-252-991A-24494
24	64.5	18.0	244	4	US-09-461-325-463
25	64.5	18.0	244	4	US-10-012-542-463
26	64.5	18.0	244	4	US-10-115-123-463
27	63.5	17.7	240	4	US-09-152-060-100

28	63.5	17.7	335	4	US-09-152-060-64	Sequence 64, Appl
29	63.5	17.7	391	3	US-08-706-216-6	Sequence 6, Appl
30	63.5	17.7	391	4	US-09-650-284B-6	Sequence 6, Appl
31	63	17.5	850	4	US-09-915-181A-3	Sequence 3, Appl
32	62	17.3	541	4	US-09-538-092-347	Sequence 347, App
33	62	17.3	602	4	US-09-248-796A-16684	Sequence 16684, A
34	62	17.3	737	4	US-09-583-110-4038	Sequence 4038, Ap
35	62	17.3	742	4	US-09-107-433-3626	Sequence 3626, Ap
36	61	17.0	448	4	US-09-248-796A-14116	Sequence 14116, A
37	61	17.0	522	4	US-09-248-796A-14121	Sequence 14121, A
38	60.5	16.9	854	2	US-09-070-060-4	Sequence 4, Appl
39	60.5	16.9	854	3	US-09-357-746-4	Sequence 4, Appl
40	60	16.7	642	4	US-09-248-796A-16106	Sequence 16106, A
41	60	16.7	1037	4	US-09-428-711A-21	Sequence 21, Appl
42	58.5	16.3	1060	4	US-09-248-796A-16624	Sequence 16624, A
43	58.5	16.3	1093	3	US-08-545-860D-55	Sequence 55, Appl
44	58.5	16.3	1093	5	PCT-US94-04496-55	Sequence 55, Appl
45	58.5	16.3	3256	4	US-09-919-172-98	Sequence 98, Appl

#### ALIGNMENTS

RESULT 1  
US-08-752-891-2  
Sequence 2, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-752-891-2  
Query Match 100.0%; Score 359; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QSPFLTIQSNTHHTQSSSSSDGGLFRSRPAHSLPPGHDGVEPYVDFAEFTRLMSVDHG 60
Db 437 QSPFLTIQSNTHHTQSSSSSDGGLFRSRPAHSLPPGHDGVEPYVDFAEFTRLMSVDHG 496
QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 2
US-08-752-891-6
; Sequence 6, Application US/08752891
; Patent No. 5837819
; GENERAL INFORMATION:
; APPLICANT: MATSUMOTO, Kunihiko
; APPLICANT: NISHIDA, Hisuke
; TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,891
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-300856
; FILING DATE: 28-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-126282
; FILING DATE: 24-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17981/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-752-891-6

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFLTIQSNTHHTQSSSSSDGGLFRSRPAHSLPPGHDGVEPYVDFAEFTRLMSVDHG 60
Db 437 QSPFLTIQSNTHHTQSSSSSDGGLFRSRPAHSLPPGHDGVEPYVDFAEFTRLMSVDHG 496
QY 61 EQSVVTAP 68
Db 497 EQSVVTAP 504

RESULT 3
US-09-144-178-2
Sequence 2, Application US/09144178

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? Patent No. 5989862
? GENERAL INFORMATION:
? APPLICANT: MATSUMOTO, Kunihiko
? APPLICANT: NISHIDA, Eisuke
? TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20007-5109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/144,178
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/752,891
? FILING DATE: 20-NOV-1996
? APPLICATION NUMBER: JP 8-300856
? FILING DATE: 28-OCT-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 8-126282
? FILING DATE: 24-APR-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 17981/111
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)672-5300
? TELEFAX: (202)672-5399
? TELEX: 904136
? INFORMATION FOR SEQ. ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 504 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-144-178-2

Query Match 100.0%; Score 359; DB 2; Length 504;
Best Local Similarity 100.0%; Pred. No. 4,6e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 QSPFTLQSTNTHHTSSSSSDGGLFSSRPASHLPPEGDORVPPYDFAEFRLMSVDHG 60
DB 437 QSPFTLQSTNTHHTSSSSSDGGLFSSRPASHLPPEGDGVPPYDFAEFRLMSVDHG 496
QY 61 EGSVVTAP 68
DB 497 EGSVVTAP 504

RESULT 4
US-09-144-178-6
? Sequence 6, Application US/09144178
? Patent No. 5989862
? GENERAL INFORMATION:
? APPLICANT: MATSUMOTO, Kunihiko
? APPLICANT: NISHIDA, Eisuke
? TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.

```

COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,178  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-144-178-6

Query Match 100.0%; Score 359; DB 2; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTGOSTVHTHTQSSSSSDGGLFRSRPAHSILPPGSDGVEVPYDPAEFRLMSVDHG 60  
DB 437 QSPFTLTGOSTVHTHTQSSSSSDGGLFRSRPAHSILPPGSDGVEVPYDPAEFRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 5  
US-09-406-854-2  
Sequence 2, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-406-854-2

Query Match 100.0%; Score 359; DB 3; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTGOSTVHTHTQSSSSSDGGLFRSRPAHSILPPGSDGVEVPYDPAEFRLMSVDHG 60  
DB 437 QSPFTLTGOSTVHTHTQSSSSSDGGLFRSRPAHSILPPGSDGVEVPYDPAEFRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 6  
US-09-406-854-6  
Sequence 6, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 504 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-854-6

Query Match 100.0%; Score 359; DB 3; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 496

QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 7

US-09-529-279-2

Sequence 2, Application US/09529279

Patent No. 6451617

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT FILING DATE: US/09/529, 279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 504

TYPE: PRT

ORGANISM: Homo sapiens

US-09-529-279-2

Query Match 100.0%; Score 359; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 496

QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 8

US-10-158-895-2

Sequence 2, Application US/10158895

Patent No. 6551840

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT APPLICATION NUMBER: US/10/158, 895

CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: US/09/529, 279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 504

TYPE: PRT

ORGANISM: Homo sapiens

US-10-158-895-2

Query Match 100.0%; Score 359; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 496

QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 9

US-09-529-279-43

Sequence 43, Application US/09529279

Patent No. 6451617

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES

FILE REFERENCE: 053466/0278

CURRENT FILING DATE: US/09/529, 279

PRIOR FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: PCT/JP98/04796

PRIOR FILING DATE: 1998-10-22

PRIOR APPLICATION NUMBER: JP 9/290188

PRIOR FILING DATE: 1997-10-22

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 43

LENGTH: 513

TYPE: PRT

ORGANISM: Homo sapiens

US-09-529-279-43

Query Match 100.0%; Score 359; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 4.7e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 60  
DB 446 QSPFTLTQSTNTHTQSSSSSDGGLFRSRPAHSILPGEEDGRVEPYVDFAEFYRLMSVDHG 505

QY 61 EQSVVTAP 68  
DB 506 EQSVVTAP 513

RESULT 10

US-10-158-895-43

Sequence 43, Application US/10158895

Patent No. 6551840

GENERAL INFORMATION:

APPLICANT: ONO, KOICHIRO

APPLICANT: OHTOMO, TOSHIHIKO

```

; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-43

Query Match      100.0%; Score 359; DB 4; Length 513;
Best Local Similarity 100.0%; Pred. No. 4.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
DB 446 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 505

OY 61 EOSVVTAP 68
DB 506 EOSVVTAP 513

RESULT 11
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-11

Query Match      100.0%; Score 359; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
DB 437 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496

OY 61 EOSVVTAP 68
DB 497 EOSVVTAP 504

RESULT 12
US-10-158-895-11
; Sequence 11, Application US/10158895
; Patent No. 6551640
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; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-895-11

Query Match      100.0%; Score 359; DB 4; Length 517;
Best Local Similarity 100.0%; Pred. No. 4.7e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 60
DB 437 OSPTLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVEPYVDFAEFYRLMSVDHG 496

OY 61 EOSVVTAP 68
DB 497 EOSVVTAP 504

RESULT 13
US-09-529-279-41
; Sequence 41, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; CURRENT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-529-279-41

Query Match      21.4%; Score 77; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OSPTLTQSTNTHTQ 15
DB 2 OSPTLTQSTNTHTQ 16

RESULT 14
US-10-158-895-41
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; Sequence 41, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-158-895-41
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Query Match          21.4%; Score 77; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 QSPPLTQSTNTHTQ 15
Db      2 QSPPLTQSTNTHTQ 16
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RESULT 15
US-09-902-540-16476
; Sequence 16476, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16476
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16476
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Best Local Similarity 29.0%; Pred. No. 0.61;
Matches 18; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
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Db      420 VTMERLVNVARGGCVLTMTMKKATDYEDLPFGAGARVMDFDVLYERYRA-AYEHQQLAN 478
QY      65 VT 66
Db      479 VT 480
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Search completed: August 2, 2005, 20:34:07  
Job time : 9.27027 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2005, 20:29:48 ; Search time 25.0405 Seconds

(without alignments)  
1058.018 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359  
Sequence: 1 QSTPLTQSTNTHTQSSSSS.....AEFRYLMVHGEGSVYTP 68

Scoring table: BLOSUM62  
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Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 1745140

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	359	100.0	504	13	US-10-123-427-6
3	359	100.0	504	13	US-10-158-895-2
4	359	100.0	504	13	US-10-158-895-2
5	359	100.0	504	16	US-10-820-583A-10
6	359	100.0	513	13	US-10-158-895-43
7	359	100.0	513	13	US-10-384-743-43
8	359	100.0	517	13	US-10-158-895-11
9	359	100.0	517	13	US-10-384-743-11
10	352	98.1	84	9	US-09-925-300-1270
11	77	21.4	16	13	US-10-158-895-41

12	77	21.4	16	14	US-10-384-743-41	Sequence 41, Appl
13	75.5	21.0	64	15	US-10-369-493-19278	Sequence 19278, A
14	70.5	19.6	87	15	US-10-425-115-271372	Sequence 271372, A
15	70	19.5	147	15	US-10-424-599-225143	Sequence 225143, A
16	70	19.5	238	16	US-10-437-963-119398	Sequence 119398, A
17	69.5	19.4	199	9	US-09-941-831-21	Sequence 21, Appl
18	68.5	19.1	213	16	US-10-425-115-305401	Sequence 305401, A
19	67.5	18.8	739	14	US-10-097-534-10	Sequence 10, Appl
20	67.5	18.8	739	15	US-10-374-937A-89	Sequence 89, Appl
21	67.5	18.8	739	15	US-10-182-936A-89	Sequence 89, Appl
22	67.5	18.8	739	16	US-10-477-238A-668	Sequence 668, App
23	67.5	18.8	739	17	US-10-680-287A-668	Sequence 668, App
24	67.5	18.8	739	16	US-10-477-173-668	Sequence 668, App
25	67.5	18.8	752	10	US-09-919-039-235	Sequence 235, App
26	67.5	18.8	903	17	US-10-489-740-145	Sequence 145, App
27	67	18.7	170	16	US-10-767-701-61071	Sequence 61071, A
28	66	18.4	16	13	US-10-158-895-40	Sequence 40, Appl
29	66	18.4	16	14	US-10-384-743-40	Sequence 40, Appl
30	65.5	18.2	498	13	US-10-037-667-5	Sequence 5, Appl
31	65.5	18.2	498	18	US-10-885-227-44	Sequence 44, Appl
32	64.5	18.0	244	14	US-10-115-123-463	Sequence 463, App
33	64.5	18.0	244	14	US-10-115-123-463	Sequence 463, App
34	64.5	18.0	244	18	US-10-800-834-463	Sequence 463, App
35	63.5	17.7	240	9	US-09-853-161-100	Sequence 100, App
36	63.5	17.7	240	9	US-09-852-659A-100	Sequence 100, App
37	63.5	17.7	240	9	US-09-852-797-100	Sequence 100, App
38	63.5	17.7	240	15	US-10-058-993-100	Sequence 100, App
39	63.5	17.7	335	9	US-09-853-161-64	Sequence 64, Appl
40	63.5	17.7	335	9	US-09-852-659A-64	Sequence 64, Appl
41	63.5	17.7	335	9	US-09-852-797-64	Sequence 64, Appl
42	63.5	17.7	335	15	US-10-058-993-64	Sequence 64, Appl
43	63.5	17.7	824	14	US-10-226-844-1	Sequence 1, Appl
44	63.5	17.7	824	14	US-10-210-951-58	Sequence 58, Appl
45	63.5	17.7	824	14	US-10-211-884-58	Sequence 58, Appl

#### ALIGNMENTS

RESULT 1  
US-10-123-427-2  
Sequence 2, Appl  
Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunhiro  
NISHIDA, Eisuke  
TITLE OF INVENTION: TAI1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-123-427-2

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 2  
US-10-123-427-6  
Sequence 6, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 504 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-123-427-6

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 3  
US-10-158-895-2  
Sequence 2, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-2

Query Match 100.0%; Score 359; DB 13; Length 504;  
Best Local Similarity 100.0%; Pred. No. 3.3e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLTGNTHTQSSSSSDGGLFRSRPAHSLPPGEDGRVPEYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 4  
US-10-384-743-2  
Sequence 2, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 504  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-2

Query Match  
Best Local Similarity 100.0%; Score 359; DB 14; Length 504;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 437 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFYRLMSVDHG 496  
QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 5  
US-10-820-583A-10  
Sequence 10, Application US/10820583A  
Publication No. US20040242461A1  
GENERAL INFORMATION:  
APPLICANT: Schneider, Michael  
APPLICANT: Oh, Hidemasa  
TITLE OF INVENTION: Modulators of Telomere Stability  
FILE REFERENCE: HO-P02673US1  
CURRENT APPLICATION NUMBER: US/10/820,583A  
PRIOR FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 60/461,095  
PRIOR FILING DATE: 2003-04-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 504  
TYPE: PRT  
ORGANISM: HUMAN  
US-10-820-583A-10

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Best Local Similarity 100.0%; Score 359; DB 16; Length 504;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 6  
US-10-158-895-43  
Sequence 43, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
PRIOR FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-158-895-43

Query Match  
Best Local Similarity 100.0%; Score 359; DB 13; Length 513;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EQSVVTAP 68  
DB 506 EQSVVTAP 513

RESULT 7  
US-10-384-743-43  
Sequence 43, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
PRIOR FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 513  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-743-43

Query Match  
Best Local Similarity 100.0%; Score 359; DB 14; Length 513;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFYRLMSVDHG 60  
DB 446 QSPFLTQSTNTHTQSSSSSDGGLFRSRPAHSLPPGDDGVEPYVDFAEFYRLMSVDHG 505  
QY 61 EQSVVTAP 68  
DB 506 EQSVVTAP 513

RESULT 8  
US-10-158-895-11  
Sequence 11, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIIKO  
APPLICANT: TSUCHIYA, MASAYUKI

;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/158,895  
;; CURRENT FILING DATE: 2002-06-03  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: PCT/US00/05988  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 517  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-158-895-11

Query Match 100.0%; Score 359; DB 13; Length 517;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 496  
OY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 9  
US-10-384-743-11  
;; Sequence 11, Application US/10384743  
;; Publication No. US2003016228A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ONO, KOICHIRO  
;; APPLICANT: OHTOMO, TOSHIHIKO  
;; APPLICANT: TSUCHIYA, MASAYUKI  
;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/384,743  
;; CURRENT FILING DATE: 2003-03-11  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: JP 9/290188  
;; PRIOR FILING DATE: 1997-10-22  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 517  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-384-743-11

Query Match 100.0%; Score 359; DB 14; Length 517;  
Best Local Similarity 100.0%; Pred. No. 3.4e-34;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 60  
DB 437 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 496  
OY 61 EQSVVTAP 68  
DB 497 EQSVVTAP 504

RESULT 10  
US-09-925-300-1270  
;; Sequence 1270, Application US/09925300

;; Patent No. US20020151681A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Craig Rosen,  
;; APPLICANT: Steve Ruben,  
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
;; FILE REFERENCE: PA101  
;; CURRENT APPLICATION NUMBER: US/09/925,300  
;; CURRENT FILING DATE: 2001-08-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/05988  
;; PRIOR FILING DATE: 2000-03-08  
;; PRIOR FILING DATE: 1999-03-12  
;; PRIOR APPLICATION NUMBER: 60/124,270  
;; NUMBER OF SEQ ID NOS: 1890  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1270  
;; LENGTH: 84  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (38)  
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1270

Query Match 98.1%; Score 352; DB 9; Length 84;  
Best Local Similarity 98.5%; Pred. No. 2.6e-34;  
Matches 67; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 60  
DB 17 QSPFTLQSTNTHQSSSSSDGGLFRSRPAHSLPPGDEGRVPEYVDFAEFYRLMSVDHG 76  
OY 61 EQSVVTAP 68  
DB 77 EQSVVTAP 84

RESULT 11  
US-10-158-895-41  
;; Sequence 41, Application US/10158895  
;; Publication No. US20020155624A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ONO, KOICHIRO  
;; APPLICANT: OHTOMO, TOSHIHIKO  
;; APPLICANT: TSUCHIYA, MASAYUKI  
;; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
;; FILE REFERENCE: 053466/0278  
;; CURRENT APPLICATION NUMBER: US/10/158,895  
;; CURRENT FILING DATE: 2002-06-03  
;; PRIOR APPLICATION NUMBER: US/09/529,279  
;; PRIOR FILING DATE: 2000-04-11  
;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: JP 9/290188  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 41  
;; LENGTH: 16  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-158-895-41

Query Match 21.4%; Score 77; DB 13; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QSPFTLQSTNTHQ 15  
DB 2 QSPFTLQSTNTHQ 16

RESULT 12  
US-10-384-743-41  
; Sequence 41, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHITAKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384,743  
; CURRENT FILING DATE: 2003-03-11/529,279  
; PRIOR APPLICATION NUMBER: US/09/529,279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; US-10-384-743-41

Query Match 21.4%; Score 77; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSPPLTQSTNTHTQ 15  
DB 2 QSPPLTQSTNTHTQ 16

RESULT 13  
US-10-369-493-19278  
; Sequence 19278, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 19278  
; LENGTH: 641  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
; US-10-369-493-19278

Query Match 21.0%; Score 75.5; DB 15; Length 641;  
Best Local Similarity 29.0%; Pred. No. 4.1;  
Matches 18; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 5 LTLQSTNTHTQSSSSSDGGLFRSRPAHSLPPGEGRVEPYDFAEFYRLMSVDHGEQSV 64  
DB 418 VTMLRNLVHARGEGVTLMTVMKKATDYEDLPFGAGARVMDFDLVERVRA-AYEHGQLAN 476  
QY 65 VT 66

DB 477 VT 478

RESULT 14  
US-10-425-115-271372  
; Sequence 271372, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 271372  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_179086C.1.pep  
; US-10-425-115-271372

Query Match 19.6%; Score 70.5; DB 16; Length 87;  
Best Local Similarity 32.3%; Pred. No. 1.5;  
Matches 21; Conservative 4; Mismatches 19; Indels 21; Gaps 3;

QY 7 LQSTNTHTQSSSSSDGGLFRSRPAHSLP-----PGEDGRVEPYD 47  
DB 5 LAAENTHT--QAQGGGRRLHLIFRRRTKSTYPLHWRUDWTKGKAPSTDGAPVYV 62  
QY 48 FAEFY 52  
DB 63 LASFY 67

RESULT 15  
US-10-424-599-225143  
; Sequence 225143, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 225143  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_45334C.1.pep  
; US-10-424-599-225143

Query Match 19.5%; Score 70; DB 15; Length 147;  
Best Local Similarity 29.9%; Pred. No. 3.2;  
Matches 23; Conservative 8; Mismatches 24; Indels 22; Gaps 3;

QY 3 PTLTQSTNTHTQSSSSSDGGL-----FRSRPAHSLPPGED-----GRVEPY 45  
DB 11 PTLTFLGRSRNNNNSSSSAASRIHFRRISISAMSTPGSSSDASTKTRVYIKGRVQ-- 68  
QY 46 VDFAEFYRLMSVDHGEQ 62

Wed Aug 3 09:50:51 2005

us-09-830-144-4\_copy\_437\_504.rapb

Page 6

Db 69 ---GVFYNWTFIENATQ 82

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Job time : 25.0405 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 2, 2005, 20:33:39 ; Search time 68.4595 Seconds

(without alignments)  
1625.295 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359  
Sequence: 1 QSTPLTLQSTNTHTQSSSS.....AEFYRLMSVDHGDSVTAP 68

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=PCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued\_Patents\_NA: \*  
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4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCUTS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	359	100.0	1560	2	US-08-752-891-1
2	359	100.0	1560	2	US-08-752-891-5
3	359	100.0	1560	2	US-09-144-178-1
4	359	100.0	1560	2	US-09-144-178-5
5	359	100.0	1560	3	US-09-406-854-1
6	359	100.0	1560	3	US-09-406-854-5
7	359	100.0	1560	3	US-09-529-279-1
8	359	100.0	1560	4	US-10-158-895-1
9	359	100.0	1568	4	US-09-529-279-42
10	359	100.0	1568	4	US-10-158-895-42
11	359	100.0	1569	3	US-09-529-279-10
12	359	100.0	1569	4	US-10-158-895-10

13	75.5	21.0	2076	4	US-09-902-540-9325	Sequence 9325, App
14	75.5	21.0	9839	4	US-09-902-540-996	Sequence 996, App
15	71.5	19.9	1108	5	PCT-US93-03035-1	Sequence 1, Appl1
C 16	69	19.2	44998	4	US-09-949-016-12824	Sequence 12824, A
C 17	69	19.2	44999	4	US-09-949-016-14832	Sequence 14832, A
C 18	69	19.2	44999	4	US-09-949-016-14833	Sequence 14833, A
C 19	69	19.2	44999	4	US-09-949-016-17109	Sequence 17109, A
C 20	69	19.2	44999	4	US-09-949-016-17109	Sequence 17109, A
21	68	18.9	146307	4	US-09-949-016-14881	Sequence 14881, A
22	68	18.9	146307	4	US-09-949-016-14882	Sequence 14882, A
23	68	18.9	146307	4	US-09-949-016-14883	Sequence 14883, A
24	68	18.9	146307	4	US-09-949-016-14884	Sequence 14884, A
25	68	18.9	146307	4	US-09-949-016-14885	Sequence 14885, A
26	68	18.9	146307	4	US-09-949-016-12836	Sequence 12836, A
27	68	18.9	146307	4	US-09-949-016-12837	Sequence 12837, A
28	68	18.9	146307	4	US-09-949-016-14888	Sequence 14888, A
29	68	18.9	148405	4	US-09-949-016-11747	Sequence 11747, A
30	68	18.9	148405	4	US-09-949-016-12835	Sequence 12835, A
31	68	18.9	148405	4	US-09-949-016-12836	Sequence 12836, A
32	68	18.9	148405	4	US-09-949-016-12837	Sequence 12837, A
33	67.5	18.8	2559	2	US-09-070-060-2	Sequence 2, Appl1
34	67.5	18.8	2559	3	US-09-357-746-2	Sequence 234, App
35	67.5	18.8	2678	4	US-09-919-039-234	Sequence 1, Appl1
36	67.5	18.8	5359	2	US-09-070-060-1	Sequence 15731, A
37	67.5	18.8	5372	3	US-09-357-746-1	Sequence 15731, A
C 38	67	18.7	19161	4	US-09-949-016-15731	Sequence 15731, A
C 39	67	18.7	42898	4	US-09-949-016-15904	Sequence 15904, A
C 40	67	18.7	42898	4	US-09-949-016-15904	Sequence 15904, A
41	66.5	18.5	1275	4	US-09-248-796A-408	Sequence 408, App
42	66	18.4	601	4	US-09-949-016-56557	Sequence 56557, A
43	66	18.4	601	4	US-09-949-016-59181	Sequence 59181, A
44	66	18.4	43537	4	US-09-949-016-13458	Sequence 13458, A
45	66	18.4	636591	4	US-09-949-016-11808	Sequence 11808, A

#### ALIGNMENTS

RESULT 1  
US-08-752-891-1  
Sequence 1, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-08-752-891-1

Alignment Scores:  
Pred. No.: 3,91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-08-752-891-1 (1-1560)

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DB 1338 CAAAGCCCGACCTTAACCTTGACATGCCAACACGACACGACGACACGACCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40  
DB 1398 TCTGACGAGGCGCTCTCCGCTCCCGGCCACCTCGCTCCGCTGCGGAGAGCGGT 1457  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGAGCCCTTAATGAGACTTGTGAGTTTACCGGCTCTGAGACGTGAGACCATGGC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 2  
US-08-752-891-5

Sequence 5, Application US/08752891  
Patent No. 5837819  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282

FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-08-752-891-5

Alignment Scores:  
Pred. No.: 3,91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-08-752-891-5 (1-1560)

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DB 1338 CAAAGCCCGACCTTAACCTTGACATGCCAACACGACACGACGACGACCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40  
DB 1398 TCTGACGAGGCGCTCTCCGCTCCCGGCCACCTCGCTCCGCTGCGGAGAGCGGT 1457  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGAGCCCTTAATGAGACTTGTGAGTTTACCGGCTCTGAGACGTGAGACCATGGC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGTGTGACAGCACCG 1541

RESULT 3

US-09-144-178-1  
Sequence 1, Application US/09144178  
Patent No. 5989862  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko  
APPLICANT: NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,178  
FILING DATE:



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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-144-178-1
US-09-144-178-1

Alignment Scores:
Pred. No.: 3,91e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 2

US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-1 (1-1560)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 1338 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
DB 1398 TCTAAGGAGGCGCTCTCCGCTCCGCGCCGCCCACTGCTCCCGCTGGGAGGACCGT 1457
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTTPSerValAspHisGly 60
DB 1458 CGTGTGAGCCCTTAAGTGAAGCTTGCTGAGTTTACCGCTCTGAGCGGTGACCATGCGC 1517
QY 61 GluGlnSerValValThrAlaPro 68
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

RESULT 4
US-09-144-178-5
Sequence 5, Application US/09144178
Patent No. 598962
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiko
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,178
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,891
FILING DATE: 20-NOV-1996
APPLICATION NUMBER: JP 8-300856
FILING DATE: 28-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-126282
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17981/111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1541
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 30..1541
US-09-144-178-5
US-09-144-178-5

Alignment Scores:
Pred. No.: 3,91e-37 Length: 1560
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 2

US-09-830-144-4_COPY_437_504 (1-68) x US-09-144-178-5 (1-1560)
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20
DB 1338 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 1397
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGluAspGly 40
DB 1398 TCTAAGGAGGCGCTCTCCGCTCCGCGCCGCCCACTGCTCCCGCTGGGAGGACCGT 1457
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTTPSerValAspHisGly 60
DB 1458 CGTGTGAGCCCTTAAGTGAAGCTTGCTGAGTTTACCGCTCTGAGCGGTGACCATGCGC 1517
QY 61 GluGlnSerValValThrAlaPro 68
DB 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

RESULT 5
US-09-144-854-1
Sequence 1, Application US/09406854
Patent No. 614062
GENERAL INFORMATION:
APPLICANT: MATSUMOTO, Kunihiko
APPLICANT: NISHIDA, Eisuke
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR
```

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-1  
Alignment Scores:  
Pred. No.: 3.91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-406-854-1 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
Db 1338 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACACGAGGACGAGCTCCAGC 1397  
QY 21 SerAepGlyGlyLeuPheAArgSerArgProAlaHisSerLeuProGlyGlyAepGly 40  
Db 1398 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACCTCGCTCCGCGAGGAGCGGT 1457  
QY 41 ArgValGluProThrValAlaPhePheAlaGluPheThrArgLeuThrSerValAlaPheSgly 60  
Db 1458 CGTGTGACGCCCTTAATGTGACCTTGTCTGAGTTTACCGCTCTGAGCGTGTGACCATGAC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
Db 1518 GAGCAGAGCGGTGTGACGACGACCG 1541

RESULT 6  
US-09-406-854-5  
Sequence 5, Application US/09406854  
Patent No. 6140042  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihito  
TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-NOV-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
US-09-406-854-5  
Alignment Scores:  
Pred. No.: 3.91e-37 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-406-854-5 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
Db 1338 CAAAGCCGACCTTAACCTGCGAGTCCACCAACGACACGAGGACGAGCTCCAGC 1397  
QY 21 SerAepGlyGlyLeuPheAArgSerArgProAlaHisSerLeuProGlyGlyAepGly 40  
Db 1398 TCTGACGAGGAGCTCTCCGCTCCGCGCCGACCTCGCTCCGCGAGGAGCGGT 1457

QY	41	ArgValGluPrcrPrrValAspPheIactIubPheTrgLeuTPsSerValAspHisGly	60
DB	1458	CGTGTTGAGCCCTAIGTGGACCTTCCTGAGTTTACCCGCTCTGGAGCTGGACCAATGC	1517
QY	61	GluGlnSerValValThrAlaPro	68
DB	1518	GAGCGAGAGCTGGTGTACAGCACCG	1541

RESULT 7  
US-09-529-279-1  
; Sequence 1, Application US/09529279

```

1  APPLICANT: ONO, KOICHIRO
2  APPLICANT: OHTOMO, TOSHITOMO
3  APPLICANT: TSUCHIYA, MASAYUKI
4  TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
5  FILE REFERENCE: 053466/0278
6  CURRENT APPLICATION NUMBER: US/09/529, 279
7  CURRENT FILING DATE: 2000-04-11
8  PRIOR APPLICATION NUMBER: PCT/JP98/04796
9  PRIOR FILING DATE: 1998-10-22
10 PRIOR APPLICATION NUMBER: JP 9/290188
11 PRIOR FILING DATE: 1997-10-22
12 NUMBER OF SEQ ID NOS: 48
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 1
15 LENGTH: 1560
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (30)..(1541)
21 US-09-529-279-1

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Alignment Scores:	
Pred. No.:	3,91e-37
Score:	359.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	3
Length:	1560
Matches:	68
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-830-144-4 COPY 437 504 (1-68) X US-09-529-279-1 (1-1560)

QY	1	GInSerProThLeuThLeuGInSerThraThTrHsrThGInSerSerSerSer	20
DB	1338	CAAAACCCGACCTTAACCTTGAGTCCACCAACGACACGCAAGAGAGAGCTCCAGC	1397
QY	21	SeArSpGlyGlyLeuPheArgSerArProAlaHisSerLeuProGlyValuAspGly	40
DB	1398	TTTGAACGAGGACTCTTCGCTCCCGAGCCGCCACTGCTCCGCTCGGGGAGGACGCT	1457
QY	41	ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly	60
DB	1458	CGGTGTGAGCCCTAATGTGACTTTGCTGTGATTTACCGGCTCTGAGCGTGGACCATGCG	1517
QY	61	GluGInSerValValThrAlaPro	68
DB	1518	GAGCAGAGCGCTGTACAGCACCG	1541

```

RESULT 8
US-10-158-895-1
; Sequence 1, Application US/10158895
; Patent No. 6551840
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/10/158,895
; CURRENT FILING DATE: 2002-06-03

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1  PRIOR APPLICATION NUMBER: US/09/529, 279
2  PRIOR FILING DATE: 2000-04-11
3  PRIOR APPLICATION NUMBER: PCT/JP98/04796
4  PRIOR FILING DATE: 1998-10-22
5  PRIOR APPLICATION NUMBER: JP 9/290188
6  PRIOR FILING DATE: 1997-10-22
7  NUMBER OF SEQ ID NOS: 48
8  SOFTWARE: Patentin Ver. 2.1
9  SEQ ID NO 1
10 LENGTH: 1560
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (30)..(1541)
16 US-10-158-895-1

```

Alignment scores:	
Pred. No.:	3,91e-37
Score:	359.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	4
Gaps:	0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-1 (1-1560)

QY	1	GLINSEPR	PROTHIRLEU	THIRLEU	GINSE	THIRAS	THIRHIS	THIRGIN	INSE	SESE	SESE	20
Db	1338	CAAGCCCG	CACTTAA	CCCTTG	CACTCC	CAAC	CGCAC	CGCAG	CAGAC	GA	CGCTCC	AGC 1397
QY	21	SERAS	PGIY	GLYLEU	PHARG	SE	ARG	SE	ARG	PRO	LAHIS	SE
Db	1398	TCTGAC	GAGG	CCCTT	CCGCT	CCCCG	CGCC	CACT	CGCT	CCCG	CGTGG	GA
QY	41	ARG	VAL	GIU	PRO	TYR	VAL	ASP	PH	EA	GLU	PH
Db	1458	COTG	TGAG	CCCT	TAN	GGA	CTTTG	CTGA	GTTC	ATAC	CGCC	CT
QY	61	GLU	GIN	SE	VAL	VAL	TH	LA	PRO			68
Db	1518	GAG	CAG	AGC	GTG	TG	AC	AG	CA	CG		1541

RESULT 9  
US-09-529-279-42  
; Sequence 42, Application US/09529279

```

1  APPLICANT: ONO, KOICHIRO
2  APPLICANT: OTOMO, TOSHITOMO
3  APPLICANT: TSUCHIYA, MASAYUKI
4  TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
5  FILE REFERENCE: 053466/0278
6  CURRENT APPLICATION NUMBER: US/09/529, 279
7  CURRENT FILING DATE: 2000-04-11
8  PRIOR APPLICATION NUMBER: PCT/JP98/04796
9  PRIOR FILING DATE: 1998-10-22
10 PRIOR APPLICATION NUMBER: JP 9/290188
11 PRIOR FILING DATE: 1997-10-22
12 NUMBER OF SEQ ID NOS: 48
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 42
15 LENGTH: 1568
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (11)..(1549)
21
22 US-09-529-279-42

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Alignment scores:	
Pred. No.:	3.94e-37
Score:	359.00
	Length: 1568
	Matches: 68



PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7)..(1557)  
US-10-158-895-10

Alignment Scores:  
Pred. No.: 3.94e-37 Length: 1569  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-10 (1-1569)

QY 1 GlnSerProThrLeuThrIleGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20  
DB 1315 CAAAGCCGAGCCTTAACCTGCACTCCACCAACGACGACGACGACGACGCTCCAGC 1374  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40  
DB 1375 TCTGACGAGGCGCTCTTCCGCTCCCGCCGCCCACTGCTCCCGCTGAGAGACGCT 1434  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGly 60  
DB 1435 CGTGTGAGCCCTATGAGACTTGTGAGATTACCGCTCTGAGAGGTTGACCATGAGC 1494

QY 61 GluGlnSerValValThrAlaPro 68  
DB 1495 GAGCAGAGCGTGTGACAGCACCG 1518

RESULT 13  
US-09-902-540-9325  
Sequence 9325, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 9325  
LENGTH: 2076  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-9325

Alignment Scores:  
Pred. No.: 6.12 Length: 2076  
Score: 75.50 Matches: 18  
Percent Similarity: 50.00% Conservative: 13  
Best Local Similarity: 29.03% Mismatches: 30  
Query Match: 21.03% Indels: 1  
DB: 4 Gaps: 1

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-902-540-9325 (1-2076)

QY 5 LeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerVal 24

DB 1258 GTGACGATGAGCGCCTGAACTTCACGCGCGGAGGCGTCACGCTGTGACGCTG 1317  
QY 25 LeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGlyArgValGluPro 44  
DB 1318 ATGAGAGAGCCACCGACTACGAGACTGCGCCCGGAGCGCGGCGGATGAGAC 1377  
QY 45 TyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGlyGlnGlnSerVal 64  
DB 1378 TTCTGTGACCTGTGTGAGCGCTACCGGCC---GCGTACAGACGACGCGCATGGCCAAC 1434  
QY 65 ValThr 66  
DB 1435 GTGACG 1440

RESULT 14  
US-09-902-540-996  
Sequence 996, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 996  
LENGTH: 9839  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-996

Alignment Scores:  
Pred. No.: 51.3 Length: 9839  
Score: 75.50 Matches: 18  
Percent Similarity: 50.00% Conservative: 13  
Best Local Similarity: 29.03% Mismatches: 30  
Query Match: 21.03% Indels: 1  
DB: 4 Gaps: 1

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-902-540-996 (1-9839)

QY 5 LeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerVal 24  
DB 6427 GTGACGATGAGCGCCTGAACTTCACGCGCGGAGGCGTCACGCTGTGACGCTG 6486  
QY 25 LeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGlyArgValGluPro 44  
DB 6487 ATGAGAGAGCCACCGACTACGAGACTGCGCCCGGAGCGCGGCGGATGAGAC 6546  
QY 45 TyrValAspPheAlaGluPheTyrArgLeuTrpSerValAspHisGlyGlnGlnSerVal 64  
DB 6547 TTCTGTGACCTGTGTGAGCGCTACCGGCC---GCGTACAGACGACGCGCATGGCCAAC 6603  
QY 65 ValThr 66  
DB 6604 GTGACG 6609

RESULT 15  
PCT-US93-03035-1/C  
Sequence 1, Application PC/TUS9303035  
GENERAL INFORMATION:  
APPLICANT: ABBOTT LABORATORIES  
TITLE OF INVENTION: PURIFIED THERMOSTABLE ENDONUCLEASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: D-377 APED, ONE ABBOTT PARK ROAD

CITY: ABBOTT PARK  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03035  
FILING DATE: 19930330  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/869,306  
FILING DATE: 16-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/860,702  
FILING DATE: 31-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BRAINARD, THOMAS D  
REGISTRATION NUMBER: 32,459  
REFERENCE/DOCKET NUMBER: 5145.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-4884  
TELEFAX: 708-937-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1108 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 114..926  
PCT-US93-03035-1

Alignment Scores:  
Pred. No.: 8.64 Length: 1108  
Score: 71.50 Matches: 15  
Percent Similarity: 70.37% Conservative: 4  
Best Local Similarity: 55.56% Mismatches: 7  
Query Match: 19.92% Indels: 1  
DB: 5 Gaps: 1

US-09-830-144-4\_COPY\_437\_504 (1-68) x PCT-US93-03035-1 (1-1108)

QY 18 SerSerSerSerApgIyGlyLeuPheArgSerArgProAlaHisSerLeuProProGly 37  
Db 203 AGCGGTGAGGCGCGAGGCGGTGCTTCACACGCGCGCCGCGCCTTTTCCCGGC 144  
QY 38 GIUAPGlyArgValGluPro 44  
Db 143 --GATGAAAGGTGGAACCC 126

Search completed: August 2, 2005, 20:47:30  
Job time : 74.4595 secs

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 2, 2005, 20:40:24 ; Search time 252.243 Seconds

(without alignments)  
1744.825 Million cell updates/sec

Title: US-09-830-144-4\_COPY\_437\_504

Perfect score: 359

Sequence: 1 QSTPLTQLQSTNTHTQSSSS.....AEFYRLMSVDHGHSVYTPAP 68

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q/cg2\_1/USPTO.spool/US09830144/funat.02082005.101156.12592/app.query.fasta\_1.654  
-DB=Published Applications NA -OPMT=fastlap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOEXT=0 -INTS-bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOLALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09830144 @CGN 1.1 1041 @funat.02082005.101156.12592  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEBUFFER -NEG\_SCORES=0 -WAIT -DSELOCK=100  
-LONGIOG -DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database : Published Applications NA.\*

1: /cg2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cg2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cg2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cg2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
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6: /cg2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cg2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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9: /cg2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
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11: /cg2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cg2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq.\*  
13: /cg2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
14: /cg2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
15: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cg2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
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18: /cg2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cg2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cg2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cg2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cg2\_6/ptodata/1/pubpna/US10I\_NEW\_PUB.seq.\*  
23: /cg2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
24: /cg2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cg2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cg2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359	100.0	1560	13 US-10-123-427-1	Sequence 1, Appli
2	359	100.0	1560	13 US-10-123-427-5	Sequence 5, Appli
3	359	100.0	1560	13 US-10-158-895-1	Sequence 1, Appli
4	359	100.0	1560	16 US-10-384-743-1	Sequence 1, Appli
5	359	100.0	1560	13 US-10-158-895-42	Sequence 42, Appli
6	359	100.0	1560	16 US-10-384-743-42	Sequence 42, Appli
7	359	100.0	1560	13 US-10-158-895-10	Sequence 10, Appli
8	359	100.0	1560	16 US-10-384-743-10	Sequence 10, Appli
9	359	100.0	3095	20 US-10-820-583A-19	Sequence 19, Appli
10	359	100.0	16877	9 US-09-764-877-3349	Sequence 3349, Ap
11	359	100.0	16877	17 US-10-242-515-3349	Sequence 3349, Ap
12	352	98.1	696	9 US-09-925-100-330	Sequence 330, App
13	346	96.4	409	10 US-09-918-995-32946	Sequence 32946, A
14	346	96.4	409	20 US-10-425-115-151890	Sequence 151890,
15	75.5	21.0	672	10 US-09-928-267-16	Sequence 16, Appli
16	75.5	21.0	833	10 US-09-928-267-8	Sequence 8, Appli
17	75.5	21.0	1923	17 US-10-369-493-42965	Sequence 42965, A
18	75	20.9	301	20 US-10-425-115-43033	Sequence 43033, A
19	75	20.9	1610	10 US-09-971-392-119	Sequence 119, App
20	73	20.3	1536	13 US-10-087-192-1532	Sequence 1532, Ap
21	72	20.1	1405	20 US-10-739-930-2095	Sequence 2095, Ap
22	72	20.1	1917	18 US-10-425-114-27016	Sequence 27016, A
23	72	20.1	2325	20 US-10-425-115-176747	Sequence 176747,
24	71.5	19.9	1797	20 US-10-425-115-79466	Sequence 79466, A
25	71.5	19.9	2616	20 US-10-425-115-79469	Sequence 79469, A
26	71	19.8	996	9 US-09-974-300-6219	Sequence 6219, Ap
27	71	19.8	48829	13 US-10-087-192-1531	Sequence 1531, Ap
28	70.5	19.6	504	20 US-10-425-115-86709	Sequence 86709, A
29	70	19.5	797	18 US-10-424-599-82301	Sequence 82301, A
30	70	19.5	1101	19 US-10-437-963-16915	Sequence 16915, A
31	69.5	19.4	1492	9 US-09-941-831-7	Sequence 7, Appli
32	69.5	19.4	9507	10 US-09-764-891-9785	Sequence 9785, Ap
33	69	19.2	1820	19 US-10-437-963-60665	Sequence 60665, A
34	69	19.2	2745	17 US-10-282-122A-31446	Sequence 31446, A
35	69	19.2	12409	10 US-09-989-442-156	Sequence 156, App
36	68.5	19.1	778	20 US-10-425-115-120738	Sequence 120738,
37	68.5	19.1	1373	20 US-10-425-115-139192	Sequence 139192,
38	68.5	19.1	1539	17 US-10-369-493-40524	Sequence 40524, A
39	68.5	19.1	1554	21 US-10-886-906-53	Sequence 53, Appli
40	68.5	19.1	3082	15 US-10-259-453-1	Sequence 1, Appli
41	68.5	19.1	3082	15 US-10-259-453-2	Sequence 2, Appli
42	68.5	19.1	16951	19 US-10-181-1748-72	Sequence 72, Appli
43	68.5	19.1	32767	16 US-10-004-113-4	Sequence 4, Appli
44	68.5	19.1	32767	17 US-10-394-948-4	Sequence 4, Appli
45	68	18.9	273	9 US-09-864-761-22569	Sequence 22569, A

## ALIGNMENTS

RESULT 1  
US-10-123-427-1  
; Sequence 1, Application US/10123427  
; Publication No. US20020119525A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUMOTO, Kunihito  
; NISHIDA, Eisuke  
; TITLE OF INVENTION: TABI PROTEIN AND DNA CODING THEREFOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-Nov-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-123-427-1  
Alignment Scores:  
Pred. No.: 4.69e-41 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-123-427-1 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCGACCTTAACCTGCACTGCAACCAACGACGACGAGACGACCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCTCTTCCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGAGACGCT 1457  
QY 41 ArgValGluProTyrValAlaPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGTGAGCCCTATGAGCTTGTGAGATTATACCGCTTGAGAGCGTGCATGCGC 1517  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1518 GAGCAGAGCGGTGTGACAGCAGCAGC 1541  
RESULT 2  
US-10-123-427-5  
Sequence 5, Application US/10123427  
Publication No. US20020119525A1  
GENERAL INFORMATION:  
APPLICANT: MATSUMOTO, Kunihiko

NISHIDA, Eisuke  
TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/123,427  
FILING DATE: 17-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,854  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US/08/752,891  
FILING DATE: 20-Nov-1996  
APPLICATION NUMBER: JP 8-300856  
FILING DATE: 28-Oct-1996  
APPLICATION NUMBER: JP 8-126282  
FILING DATE: 24-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 17981/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1560 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1541  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 30..1541  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-123-427-5  
Alignment Scores:  
Pred. No.: 4.69e-41 Length: 1560  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-123-427-5 (1-1560)  
QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1338 CAAAGCCGACCTTAACCTGCACTGCAACCAACGACGACGAGACGACCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCTCTTCCGCTCCGCGCCGCGCCACTCGCTCCGCTGCGAGACGCT 1457  
QY 41 ArgValGluProTyrValAlaPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGTGAGCCCTATGAGCTTGTGAGATTATACCGCTTGAGAGCGTGCATGCGC 1517



QY 61 GluInSerValThrAlaPro 68  
DB 1518 GAGCAGAGCGGTGTGACGACCG 1541

## RESULT 3

US-10-158-895-1  
; Sequence 1, Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158, 895  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529, 279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (30)..(1541)  
US-10-158-895-1

## Alignment Scores:

Pred. No.:	4.69e-41	Length:	1560
Score:	359.00	Matches:	68
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-1 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20  
DB 1338 CAAGGCCGAGCCTTAACCTGAGTCCACCAACGACGACGACGACGACGACGCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCGCTTCCGCTCCGCCGCCGCCGCTCCGCCCTGGCGAGGACGCT 1457  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGTGAGCCCTATGTGACCTTTCCTGAGTTTACCGCTCTGAGCGTGAACCAATGCG 1517  
QY 61 GluInSerValThrAlaPro 68  
DB 1518 GAGCAGAGCGGTGTGACGACCG 1541

RESULT 4  
US-10-384-743-1  
; Sequence 1, Application US/10384743  
; Publication No. US20030162228A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/384, 743  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US/09/529, 279  
; PRIOR FILING DATE: 2000-04-11

;; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
;; PRIOR FILING DATE: 1998-10-22  
;; PRIOR APPLICATION NUMBER: JP 9/290188  
;; PRIOR FILING DATE: 1997-10-22  
;; NUMBER OF SEQ ID NOS: 48  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 1560  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (30)..(1541)  
US-10-384-743-1

## Alignment Scores:

Pred. No.:	4.69e-41	Length:	1560
Score:	359.00	Matches:	68
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-384-743-1 (1-1560)

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20  
DB 1338 CAAGGCCGAGCCTTAACCTGAGTCCACCAACGACGACGACGACGACGCTCCAGC 1397  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1398 TCTGACGAGGCGCTTCCGCTCCGCCGCCGCCGCTCCGCCCTGGCGAGGACGCT 1457  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1458 CGGTGTGAGCCCTATGTGACCTTTCCTGAGTTTACCGCTCTGAGCGTGAACCAATGCG 1517  
QY 61 GluInSerValThrAlaPro 68  
DB 1518 GAGCAGAGCGGTGTGACGACCG 1541

## RESULT 5

US-10-158-895-42  
; Sequence 42, Application US/10158895  
; Publication No. US20020155624A1  
; GENERAL INFORMATION:  
; APPLICANT: ONO, KOICHIRO  
; APPLICANT: OHTOMO, TOSHIHIKO  
; APPLICANT: TSUCHIYA, MASAYUKI  
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
; FILE REFERENCE: 053466/0278  
; CURRENT APPLICATION NUMBER: US/10/158, 895  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/529, 279  
; PRIOR FILING DATE: 2000-04-11  
; PRIOR APPLICATION NUMBER: PCT/JP98/04796  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: JP 9/290188  
; PRIOR FILING DATE: 1997-10-22  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 1568  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (11)..(1549)  
US-10-158-895-42

Alignment Scores:  
Pred. No.: 4.72e-41 Length: 1568  
Score: 359.00 Matches: 68

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-42 (1-1568)

QY 1 GlnSerProThrLeuThrlLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1346 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGACGCTCCAGC 1405  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1406 TCTGACGAGGCGCTTCCGCTCCCGGCGCCCACTGCTCCGCGCTGGCGAGGACGGT 1465  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1466 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1526 GAGCAGAGCGGTGTGACAGCACCG 1549

## RESULT 6

US-10-384-743-42  
Sequence 42, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 1568  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1549)  
US-10-384-743-42

## Alignment Scores:

Pred. No.: 4.72e-41 Length: 1568  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-384-743-42 (1-1568)

QY 1 GlnSerProThrLeuThrlLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1346 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 1405  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1406 TCTGACGAGGCGCTTCCGCTCCCGGCGCCCACTGCTCCGCGCTGGCGAGGACGGT 1465  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1466 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1525

QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1526 GAGCAGAGCGGTGTGACAGCACCG 1549

## RESULT 7

US-10-158-895-10  
Sequence 10, Application US/10158895  
Publication No. US20020155624A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/158,895  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US/09/529,279  
PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (77)..(1557)  
US-10-158-895-10

## Alignment Scores:

Pred. No.: 4.72e-41 Length: 1569  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-158-895-10 (1-1569)

QY 1 GlnSerProThrLeuThrlLeuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1315 CAAAGCCCGACCTTAACCTTCAGTCCACCAACGACGACGACGACGCTCCAGC 1374  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGluAspGly 40  
DB 1375 TCTGACGAGGCGCTTCCGCTCCCGGCGCCCACTGCTCCGCGCTGGCGAGGACGGT 1434  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1435 CGTGTGAGCCCTATGTGAGCTTTGCTGAGTTTACCGCTCTGGAGCGTGGACCATGGC 1494  
QY 61 GlnGlnSerValValThrAlaPro 68  
DB 1495 GAGCAGAGCGGTGTGACAGCACCG 1518

RESULT 8  
US-10-384-743-10  
Sequence 10, Application US/10384743  
Publication No. US20030162228A1  
GENERAL INFORMATION:  
APPLICANT: ONO, KOICHIRO  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES  
FILE REFERENCE: 053466/0278  
CURRENT APPLICATION NUMBER: US/10/384,743  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: US/09/529,279

PRIOR FILING DATE: 2000-04-11  
PRIOR APPLICATION NUMBER: PCT/JP98/04796  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: JP 9/290188  
PRIOR FILING DATE: 1997-10-22  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7) ..(1557)  
US-10-384-743-10

Alignment Scores:  
Pred. No.: 4.72e-41 Length: 1569  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-384-743-10 (1-1569)

QY 1 GlnSerProthrIleuThrIleuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1315 CAAAGCCCGACCTTAACCTTGACGTCCACCAACGACGACGAGAGGACCTCCAGC 1374  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40  
DB 1375 TCTGACGAGGCGCTCTTCCGCTCCGCGCCCACTGCTCCGCTCGGAGGAGCGGT 1434  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1435 CGTGTGAGCCCTTAATGTGACCTTGCTGAGTTTAACTGAGCGGTGACCATGCGC 1494  
QY 61 GluGlnSerValValThrAlaPro 68  
DB 1495 GAGCAGAGCGGTGTGACGACGACCG 1518

## RESULT 9

US-10-820-583A-19  
Sequence 19, Application US/10820583A  
Publication No. US20040242461A1  
GENERAL INFORMATION:  
APPLICANT: Schneider, Michael  
TITLE OF INVENTION: Modulators of Telomere Stability  
FILE REFERENCE: HO-P02673US1  
CURRENT APPLICATION NUMBER: US/10/820,583A  
CURRENT FILING DATE: 2004-04-08  
PRIOR APPLICATION NUMBER: US 60/461,095  
PRIOR FILING DATE: 2003-04-08  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 3095  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-820-583A-19

Alignment Scores:  
Pred. No.: 1.06e-40 Length: 3095  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 20 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-820-583A-19 (1-3095)

QY 1 GlnSerProthrIleuThrIleuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 1329 CAAAGCCCGACCTTAACCTTGACGTCCACCAACGACGACGAGAGGACCTCCAGC 1388  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40  
DB 1389 TCTGACGAGGCGCTCTTCCGCTCCGCGCCCACTGCTCCGCTCGGAGGAGCGGT 1448  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 1449 CGTGTGAGCCCTTAATGTGACCTTGCTGAGTTTAACTGAGCGGTGACCATGCGC 1508  
QY 61 GluGlnSerValValThrAlaPro 68  
DB 1509 GAGCAGAGCGGTGTGACGACGACCG 1532

## RESULT 10

US-09-764-877-3349  
Sequence 3349, Application US/09764877  
Patent No. US20020147140A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC005  
CURRENT APPLICATION NUMBER: US/09/764,877  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - refer to PALM or file wrapper  
NUMBER OF SEQ ID NOS: 4031  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3349  
LENGTH: 16877  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-764-877-3349

Alignment Scores:  
Pred. No.: 7.95e-40 Length: 16877  
Score: 359.00 Matches: 68  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-764-877-3349 (1-16877)

QY 1 GlnSerProthrIleuThrIleuGlnSerThrAsnThrHisThrGlnSerSerSerSer 20  
DB 15011 CAAAGCCCGACCTTAACCTTGACGTCCACCAACGACGACGAGAGGACCTCCAGC 15070  
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40  
DB 15071 TCTGACGAGGCGCTCTTCCGCTCCGCGCCCACTGCTCCGCTCGGAGGAGCGGT 15130  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 15131 CGTGTGAGCCCTTAATGTGACCTTGCTGAGTTTAACTGAGCGGTGACCATGCGC 15190  
QY 61 GluGlnSerValValThrAlaPro 68  
DB 15191 GAGCAGAGCGGTGTGACGACGACCG 15214

## RESULT 11

US-10-242-515-3349  
Sequence 3349, Application US/10242515  
Publication No. US20040009488A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC005C1  
CURRENT APPLICATION NUMBER: US/10/242,515  
CURRENT FILING DATE: 2002-09-13  
PRIOR APPLICATION NUMBER: 09/764,877  
PRIOR FILING DATE: 2001-01-17

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; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3349

```

```

Alignment Scores:
Pred. No.: 7,95e-40 Length: 16877
Score: 359.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

```

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-242-515-3349 (1-16877)

```

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 15011 CAAAGCCGACCTTAACCTCGACGTCCACCAACGACGACGACGACGACGACGACGACG 15070
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40
Db 15071 TCTGACGAGGCGCTTCCGCTCCGCGCCGACCTCGCTCCGCTCGGACGACGCT 15130
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 15131 CGGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCGAGCGTGAACCATGGC 15190
QY 61 GlnGlnSerValValThrAlaPro 68
Db 15191 GAGCAGAGCGTGTGACGACGACCG 15214

```

```

RESULT 12
US-09-925-300-330
; Sequence 330, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
; LENGTH: 696
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (643)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (657)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (685)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-330

```

```

Alignment Scores:
Pred. No.: 1.81e-40 Length: 696
Score: 352.00 Matches: 67
Percent Similarity: 98.53% Conservative: 0
Best Local Similarity: 98.53% Mismatches: 1
Query Match: 98.05% Indels: 0
DB: 9 Gaps: 0

```

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-925-300-330 (1-696)

```

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 49 CAAAGCCGACCTTAACCTCGACGTCCACCAACGACGACGACGACGACGACGACGACG 108
QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProGlyGlyAspGly 40
Db 109 TCTRACGAGGCGCTTCCGCTCCGCGCCGACCTCGCTCCGCTCGGACGACGCT 168
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60
Db 169 CGGTGTGAGCCCTATGAGACTTGTGAGTTTACCGCTCGAGGTGAGGTGACCATGGC 228
QY 61 GlnGlnSerValValThrAlaPro 68
Db 229 GAGCAGAGCGTGTGACGACGACCG 252

```

```

RESULT 13
US-09-918-995-32946
; Sequence 32946, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: HysSeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32946
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-32946

```

```

Alignment Scores:
Pred. No.: 6.97e-40 Length: 409
Score: 346.00 Matches: 65
Percent Similarity: 97.06% Conservative: 1
Best Local Similarity: 95.59% Mismatches: 2
Query Match: 96.38% Indels: 0
DB: 10 Gaps: 0

```

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-918-995-32946 (1-409)

```

QY 1 GlnSerProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSer 20
Db 48 CAAAGCCGACCTTAACCTCGACGACCAACGACGACGACGACGACGACGACGACG 107

```

QY 21 SerAspGlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGly 40  
DB 108 TCTGACGAGAGCCCTCTCCGCTCCGCGCCGACATCGCTCCGCTCGAGAGACGGT 167  
QY 41 ArgValGluProTyrValAspPheAlaGluPheTyrArgLeuTyrSerValAspHisGly 60  
DB 168 CGTGTGAGCCCTTATGCGACTTTGCTGAGCTTTACCGCTCTGAGCGGAGACCATGGC 227  
QY 61 GluHisSerValValThrAlaPro 68  
DB 228 GAGCAGAGCGCGGTGACAGACCG 251

## RESULT 14

US-10-425-115-151890  
Sequence 151890, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 151890  
LENGTH: 406  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MET4577\_70050C.1  
US-10-425-115-151890

Alignment Scores:  
Pred. No.: 0.181 Length: 406  
Score: 78.00 Matches: 26  
Percent Similarity: 50.00% Conservative: 4  
Best Local Similarity: 43.33% Mismatches: 18  
Query Match: 21.73% Indels: 12  
DB: 20 Gaps: 3

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-10-425-115-151890 (1-406)

QY 3 ProThrLeuThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSer 22  
DB 55 CCGACTACACCC-----TCTACTGCTCGGACATCCTCTCTCTGCTGCTTCAACG 108  
QY 23 GlyGlyLeuPheArgSerArgProAlaHisSerLeuProProGlyGlyAspGlyArgVal 42  
DB 109 GGGTCCGCGCTTCGATCGCGCTCATCGAGCTCC-----GGGCCCCGAGCGGTGTC 159  
QY 43 GluProTyr-----ValAspPheAlaGluPheTyrArgLeuTyr 55  
DB 160 TCGCGTACAAATGACGCCCGGGTGGGATCTCCAGAGCGCGAGTTACCCGGTGTAC 219

## RESULT 15

US-09-928-267-16  
Sequence 16, Application US/09928267  
Publication No. US20030157705A1  
GENERAL INFORMATION:  
APPLICANT: William, Fodor  
TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND  
CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM  
FILE REFERENCE: 1087-19  
CURRENT APPLICATION NUMBER: US/09/928,267  
CURRENT FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 16  
LENGTH: 672

TYPE: DNA  
ORGANISM: porcine  
US-09-928-267-16

Alignment Scores:  
Pred. No.: 0.754 Length: 672  
Score: 75.50 Matches: 21  
Percent Similarity: 51.92% Conservative: 6  
Best Local Similarity: 40.38% Mismatches: 14  
Query Match: 21.03% Indels: 11  
DB: 10 Gaps: 2

US-09-830-144-4\_COPY\_437\_504 (1-68) x US-09-928-267-16 (1-672)

QY 6 ThrLeuGlnSerThrAsnThrHisThrGlnSerSerSerSerSerSerSerSerSerSer 25  
DB 156 ACAACGGTCGAACACACACTCAATCCAGACGTCTGCTTGAAGGCTCCAGGCCACTG 215  
QY 26 PheArgSerArgProAlaHisSerLeu-----Pro 35  
DB 216 TCAAGAGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275  
QY 36 ProGlyGlu--AspGlyArgValGluProTyrVal 46  
DB 276 CTTACTCACTGGAAGGAACTGAGATGATGAGTGTG 311

Search completed: August 2, 2005, 23:16:53  
Job time : 259.243 secs

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